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Gaps

0;

Indels

Length 741;

241

980

ASE COUNT RIGIN

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AU143295 Y79AA1 Homo sapiens cDNA clone Y79AA1001699 5', mRNA
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Bukaryota; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 739)
Ota,T., Nishikawa,T., Suzuki,Y., Ishii,S., Saito,K., Kawai,Y.,
Yamamoto,J., Wakamatsu,A., Nakamura,Y., Nagai,T., Sugano,S. and
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Pred. No. 2.4e-30;
0; Mismatches 2;
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Fax: 81-438-52-3952
                                                                                                        Matches 331; Conservative
                                                Query Match \ Best Local Similarity
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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Ota,T., Nishikawa,T., Suzuki,Y., Ishii,S., Saito,K., Kawai,Y.,
Yamamoto,J., Wakamatsu,A., Nakamura,Y., Nagai,T., Sugano,S. and
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                                                                                                                                                                                                                                                                                                                                                241 CCAACACATCCTCCGCTGCGGCGTCAGGAAGGACGACGGCACGGGGCACCGGCACCCTGTC 300
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                                                                                                                                                                        Indels
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Contact: Takao Isogai
Genomics Laboratory
Helix Research Institute
153-3 Yana Kisarazu, Chiba 292-0812, Japan
Tel: 81-438-52-3951
Fax: 81-438-52-3952
                                                                                                        Score 335.8; DB 10;
Pred. No. 3.8e-31;
0; Mismatches 2;
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AU118644.1 GI:10933771
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Best Local Similarity 99.4%;
Matches 337; Conservative
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ORGANISM

REFERENCE AUTHORS TITLE JOURNAL

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Email: genomicsthri.co.jp HRI human chNA project; 5'- & 3'-end one pass sequencing: Helix Research Institute; CDNA lbrary construction: Department of Virology, Institute of Medical Science, University of Tokyo, and 4 others Unpublished (2000)
Contact: Takao Isogai
Genomics Labratora Isogai
Helix Research Institute
1532-3 Yana, Kisarazu, Chiba 292-0812, Japan /db_xref="taxon:9666"
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BASE COUNT

source

FEATURES

Length 819,

DB 9;

Score 328.2; DB 9 Pred. No. 3.5e-30;

27.6%; 99.1%;

Query Match Best Local Similarity

860

801 aaaaggogogoggaaggggtoctgocacogogocacttggoctgoctcogtocgogog 2 AAAAGGCGCGCGGAAQGGGTCCTGCCACCGCGCCACTTGGCCTGCCTCCGTCCCGCCGC

61

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Mismatches

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Matches 330; Conservative

Length 739;

DB 9;

27.68; 99.18;

Match

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1041 catcctccgctgcggcgtcaggaaggacggcacgggaccggcaccggcaccctgtcggtatt 1100

1101 eggcatgcaggcgctacagcctgagaggtga 1133 302 CGGCATGCAGGCGCGCTACAGCCTGAGAGATGA

122 CGCCATGCCTGTGGCCGGCTCGGAGCTGCCGCCGGCCGTTGCCCCCCCGCGCGCACAGGA 181

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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 819)
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                                                                                         1041 catcotcogotgoggogtcaggaaggacgacogcacgggcaccggcacctgtcggtatt 1100
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                                                                                                                                                            Email: genomics@hri.co.jp
HRI human cDNA project; 5.- & 3'-end one pass sequencing: Helix
Wirology, Institute; CDNA library construction: Department of
Helix Research Institute.
Location/Qualifiers
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                                   Indels
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Score 328.2; DB 9
Pred. No. 3.7e-30;
0; Mismatches 3
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/cell_line="Y79"
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243 c 239 g 164 t
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/db_xref="taxon:9606"
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AU143180.1 GI:11004701
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Unpublished (2000)
Contact: Takao Isogai
Genomics Laboratory
  Matches 330; Conservative
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Email: qenomics@hri
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was primed with a NotI-oligo(dT) primer. Five prime end
cloned into the NotI and Eco Av sites of the pcMvSpORT 6
Life Technologies. Contact: Feng Liang Life pcMvSpORT 6
Life Technologies. Contact: Feng Liang Life Technologies,
a division of Invitrogen 9800 Medical Center Drive
Rockville, Maryland 20850, USA Fax: (1) 301 610 8371
http://fulllength.invitrogen.com"
233 g 152 t 9 others
                                            AL545940
AL545940 LTI_NFL006_PL2 Homo sapiens cDNA clone CSODIO23KK20 5
AL545940
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BP 191 91006 EVRY cedex - France
Email: Segref@genoscope.cns.fr, Web : www.genoscope.cns.fr,
Location/Qualifiers
1. .786
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Pred. No. 4e-30;
1; Mismatches 3;
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/db_xref="taxon:9606"
/clone="CS0DI023TK20"
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JOURNAL
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ORIGIN
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ò BAGENCOURT_6456956 NIH_MGC_92 Homo sapiens cDNA clone IMAGE:5576962 AS ', mRNA sequence. Clone="Index of the property o Eukaryota; Metazoa; Chordata: Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 985) Email: cgapbs-remail.nih.gov
Tissue Procuremit: ATCC
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at: 1041 catcotcogotgoggogtcaggaaggacgaccgcaccggcaccggcaccggtatt 1100 INTENDED THE CONTROL OF THE STATE OF THE CONTROL OF T 980 141 CAICCICCGCIGCGGCGICAGGAGGACGACGCGCGGGGGACCGGCACCGGCACCGGTAIT 300 09 921 cgccatgcctgtggccggctcggagctgcogcgccgcccccgccgccagga 26.6%; Score 315.8; DB 10; Length 985; 97.9%; Pred. No. 9.2e-29; Live 0; Mismatches 7; Indels 0; Plate: LLAM12329 row: k column: 11 High quality sequence stop: 522. Location/Qualifiers 1101 cggcatgcaggcgcgctacagcctgagaggtga 1133 /organism="Homo sapiens" /db_xref="taxon:9606" 3M466216.1 GI:18515258 Best Local Similarity 97.9 Matches 320; Conservative .985 Similarity Homo sapiens 194 BM466216 human. Query Match BASE COUNT ORIGIN DEFINITION ORGANISM REFERENCE AUTHORS TITLE JOURNAL COMMENT ACCESSION 861 VERSION FEATURES BM466216 qq δλ 셤 合 δŻ a qq ð à Ω

Technologies. Contact: Feng Liang Life Technologies, a division of Invitrogen 9800 Medical Center Drive Rockvill fliangelifetech.com URL:

**Amryland 20850, USA Fex: (1) 301 610 8371 Email: fliangelifetech.com URL:

**Attp://fullength.invitrogen.com

**208 c 192 g 126 t 3 others AL541351 AL5LEL002_PL1 Homo sapiens cDNA clone CSODE006YA08 5 prime /note-"Organ: placenta; Vector: pCMVSPORT 6; 1st strand cona was primed with a NotI-oligo(dT) primer. Five prime cond enriched, double-stranded cDNA was digested with Not and cloned into the Not I and Eco RV sites of the pcMVSPORT 6 Vector. Library was constructed by Life Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 668) 987 egeegageegegteegeegeaeggggagetgeagtacetggggeagateeaacateet 1046 0; Gaps gcctgtggccggctcggagctgccgcgccgcccccccgccgcacaggagcggga 986 Genoscope - Centre National de Sequencage BP 191 91006 EVRY cedex - France Email: seqref@genoscope.cns.fr, Web : www.genoscope.ons.fr. Location/Qualifiers 184 CGCCGAGCCGCCGCCGCCGCACGGGCAGCTGCAGTACCTGGGGCAGATCCAACATCCT Length 668; Indels Li, W.B., Gruber, C., Jessee, J. and Polayes, D. Full-length cDNA libraries and normalization Unpublished (2001) Score 310.4; DB 9; Pred. No. 4.9e-28; /organism="Homo sapiens"
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AL548721 AL548721 AL547612 AL547612

AL515911 AL515911 AL551817 AL551817 BM457044 AGENCOURT BG329382 602428522

AL556369 AL556369 AL519416 AL519416

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BM456638 1060 bp mRNA linear EST 05-FEB-2002 AGENCOURT_6408748 NIH_MGC_85 Homo sapiens cDNA clone lMAGE:5496315
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Bukaryota; Metheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1060)
11 (bases 1 to 1060)
11 MIH MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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/hote="lorgan: lymph; Vector: lymph; Vecto
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Tissue Procurement: Lou Staudt
Tissue Procurement: Lou Staudt
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
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Contact: Robert Strausberg, Ph.D.
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Contact: Takao Isogai
Genomics Laboratory
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EST 24-0CT-2000
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: genomics@hri.co.jp
HRI human cDNA project, 5'- & 3'-end one pass sequencing: Helix
Research Institute; cDNA library construction: Department of
Virology, Institute of Medical Science, University of Tokyo, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ota, T., Nishikawa, T., Suzuki, Y., Ishii, S., Saito, K., Kawai, Y., Yamamoto, J., Wakamatsu, A., Nakamura, Y., Nagai, T., Sugano, S. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1075 acgggcaccggcacctgtcggtattcggcatgcaggcgcgctacagcctgagaggtga 1133
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                                                                                                                                                                                   AU128726 AU12872 Homo sapiens CDNA clone NT2RP2004045 5', mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Helix Research Institute
153-31 Yana, Kisarazu, Chiba 292-0812, Japan
Tel: 81-438-52-3951
Fax: 81-438-52-3952
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               24.3%; Score 288.6; DB 9; 97.3%; Pred. No. 2.1e-25; Live 0; Mismatches 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Homo sapiens"
/db_xxef="taxon:9606"
/clone="NTZRP2004045"
/clone_lib="NTZRP2"
/cell_type="teratocarcinoma"
/cell_line="NT2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Helix Research Institute.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HRI human cDNA project
Unpublished (2000)
Contact: Takao Isogai
Genomics Laboratory
                                                                                                                                                                                                                                                             AUÎ28726
AU128726.1 GI:10989080
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BIS97722 905 bp mRNA linear EST 07-SEP-2001 603248376F1 NIH_MGC_96 Homo sapiens CDNA clone IMAGE:5300034 5',
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a 271 c 256 g 183 t lothers
                                                                                                                                                                                                                                                                                                             Homo sapiens
Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 905)
MIH-WGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: cgapbs-remail.nih.gov
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
cong. Library Preparation: Michael J. Brownstein (NHGRI), Shiraki
Toshiyuki and Piero Carninci (RIKEN)
CONG. Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
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/lab_host="DH108"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DNA Sequencing DY: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://imaqe.llnl.gov
Plate: LLAM11759 row: h column: 19
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98.3%; Pred. No. 3.2e-25;
Live 0; Mismatches 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                              Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
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Location/Qualifiers
1. .905
gegegetacageetgagaggtga 1133
                       323 GCGCGCTACAGCCTGAGATGA 345
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BI597722.1 GI:15490661
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Best Local Similarity 98.3
Matches 289; Conservative
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                                                                BE794349 529 bp mRNA linear EST 20-SEP-2000 601589526F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3943615 5',
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;
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                                                                                                                                                                                                                                            Dukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia: Butheria, Primates, Catarrhini, Hominidae, Homo. 1 (bases 1 to 529)
MIT-MGC http://mgc.nci.nih.gov/. National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                              CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
Plate: LLCM799 row: c column: 08
High quality sequence start: 31
High quality sequence store: 529.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone_lib="NIH_MGC_7"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pred. No. 3.4e-25;
0; Mismatches 8
                                                                                                                                                                                                                                                                                                                                                                                    Contact: Robert Strausberg, Ph.D.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /db_xref="taxon:9606"
/clone="IMAGE:3943615"
                                                                                                                                                                                                                                                                                                                                                                                                         Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP
                                                                                                                                                           BE794349.1 GI:10215534
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96.9%;
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                                                                                                                 mRNA sequence.
                                                                                                                                                                                                                                Homo sapiens
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Human nervous syst Genomic sequence # Human genomic DNA Human generic DNA Human nervous syst Human ovarian and

AAK68202 AAK81760 AAK65305 AAK65308 ABA16598 ABA16598 AAS19270 AAS19272 AAS19272 AAS14558 ABA07767 AAL0358 ABA07767 AAL0358

37449 556743 556743 220601 220916 10820 10820 10820 10820 10820 3591 9060 32169 32163 32173 38928 38928

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Copyright (c) 1993 - 2000 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       1736436 seqs, 858457221 residues
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Maximum Match 1008
Listing first 45 summaries
                                                                                                                                  - nucleic search, using sw model
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Maximum DB seq length: 200000000
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	Thymidylate syntha	Human thymidylate	Human DNA sequence	Human musculoskele	Human immune/haema	Human reproductive	DNA encoding novel	Human immune/haema	Human immune/haema
	ID	AAF31109	AAC91215	AAS94945	AAL37169	AAK65581	AAL04943	AAS84960	AAK73272	AAK73271
		22	22	24	22	22	22	23	22	22
	Match Length DB					-		1539		
Onerv	Match	98.0	98.0	24.2	17.4	17.4	17.4	17.3	17.2	17.2
	Score	1163.8	1163.8	287.2	206.8	206.8	206.4	205.8	204.6	204.6
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ບ	22	198.6	16.7	217	22	AAL03558	Human reproductive	
	23	198.6	7	38928	22	AAK68452	Human immune/haema	
	24	197.8	۲.	646	22	AAS44995	cDNA encoding nove	
	25	197.6	6	7017	22	AAL37408	Human musculoskele	
	26	197.6	6	50000	21	AAA96365	Polymorphic repeat	
υ	27	197.4	ω.	45546	20	AAX23520	Human kidney amino	
	28	196.8	16.6	97662	22	AAF83908	Genomic sequence o	
ပ	29	196.8	œ.	106746	21	AAA10225	Human PCTA-1 genom	
	30	196.6	0	7537	22	AAS36235		
	31	196.6	ا ب	7537	22	AAK65643	Human immited haema	
O	32	196.6	۰	10483	77	AAKBUBBB		
	33	196.6	ب ب	17357	22	AAK8668U	Times immine/haema	
	34	196.6	١	17363	7 6	AAK86681		
	35	136.6	٥١	18/675	7 0	AA345104		
	36	196.4	'nι	1392/	7 (AAF9/833		
υ	37	196.4	ųί	32012	77	AALU3864	Human negroduceryc	
ပ	38	196.4	<u>ر</u>	32248	77	ABAZU412	$m_{\text{max}} = m_{\text{sou}} \log s_{\text{loc}}$	
	39	196.4	J.	32248	77	AAL3/122	Times Topomia DNA	
ပ	40	196.4	'n	32248	22	AAS26/95	Hullian genomic piva	
O	41	196.4	J.	34658	77	AAK69489		
O	42	196.2	'n	1376	21	AAC99845		
υ	43	196.2	'n.	2233	22	AAK77256	n immune/	
	44	196	'n	54548	21	AAZ45596	Φ	
	45	195.8	5	16183	22	AAK74819	Human immune/haema	
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RE	RESULT	₽						
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AA AC	AA	AAF31109;						
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DE	Th	Thymidylate	synthase		coding	sequence.		
XX								
XX	An	Analyte-binding		enzyme;	analyte	yte analysis; ss.		
OS	H	Homo sapiens	Si					
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PN	_	WO200102600-A2)-A2.					
PD	11	-JAN-2001						
XX	C	0-TIM-2000.		2000ta0-tre18057	7.50			
ri X	n	-00N-200L		OTEO OM				
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XX PA		(GEAT) GEN	ATOMICS	cs.				
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E E	WP	WPI; 2001-0	2001-071583/08	.08.				
PP	AS CO	Assaying method comprises contacted binding	ethod, usef contacting binding -	ulsan	C (1)	prognosis and diagnosis of with a mutant analyte-bind	of disease, inding enzyme and	
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Matches 289; Conservative
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                                              Length 18596;
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 multiple tic syndrome and learning disorders such as dyslexia
                                                                 10; Indels
                   5605 T; 0
                                               22;
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Pred. No. 8.6e-192;
0; Mismatches 10;
                   BP; 4521 A; 3991 C; 4479 G;
                                              Query Match
Best Local Similarity 99.1%;
Matches 1176; Conservative
                    Sequence 18596
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QΥ g δŽ q QΥ g QΥ d δŽ g QYg δ q δŽ

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polynticrotics in an engine in the foat cell development such as atherosclerosis, cerebral stroke, and cardiovascular disorders such as coronary artery disease. The polynucleotide sequences can also be used as PCR primers and probes. The polynucleotides of the invention are also useful in gene therapy. Ass94746 Ass9501 represent the human polynucleotide sequences of the invention which are differentially
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Composition useful for diagnosis of conditions, disorders or diseases associated with atherosclerosis, comprises several polynucleotides that are differentially expressed in foam cell development -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present invention relates to the isolation of human polynucleotide sequences that are differentially expressed during foam cell differentiation. The polynucleotide sequences of the invention or a composition comprising these polynucleotides are useful as a high throughput method for detecting altered expression of one or more polynucleotides in a sample. The polynucleotides can be used in the
                                                                                                                                                            1157 accggoaccctgtccggtattccggcatgcaggcgcgctacagcctgagaggtgacgccgcg 1216
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cardiovascular disorder; coronary artery disease; gene therapy; ds
                                                                1037 ttgccccccgccgcacaggagcgggacgccgagccgcgcgcgcacggggagctgcag
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Ctgcccccqccqcacaggaqcggacqccgaqccgcgtccgcacggggagctgcag
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Gaps

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Indels

Length 3298;

DB 24; 4;

Score 287.2; DB 2, Pred, No. 5.8e-41; 0; Mismatches 4;

24.2%; 98.6%;

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(HUMA-) HUMAN GENOME SCI INC
                           2000US-0249207.
2000US-0249208.
2000US-0249209.
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17-NOV-2000;
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01-DEC-2000;
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06-DEC-2000;
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08-DEC-2000;
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                                                   17-NOV-
                                                                                                                         -7-NOV-7.
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Ruben SM;

Isolated polypeptide for treating, preventing and/or prognosing disorders related to the musculoskeletal system including musculoskeletal cancers and also for testing and detection e.g.

Example 2; SEQ ID NO 3534; 781pp + Sequence Listing; English.

The invention relates to novel genes (AAL34669-AAL37666) and proteins (ABB03087-ABB04109) associated with the musculoskeletal system useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. The genes are isolated from a range of human tissues disclosed in the specification. The nucleic acids, proteins, antibodies and (ant)aponists are useful in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and ovarian cancer and other cancers of the adrenal gland, bone, bone marrow, breast, gastrointestinal tract, liver, lung, or urogenital; (b) immune control canaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's disease, anutiple sclerosis, rheumatoid arthritis and ulcerative colitis; (c) cardiovascular disorders such as myccardial ischaemias; (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and epilepsy; and the finifectious diseases such as viral, bacterial, fungal and parasitic infections. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly

Sequence 9519 BP; 2702 A; 1682 C; 1664 G; 3471 T; 0 other;

ftp.wipo.int/pub/published_pct_sequences.

from WIPO at

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1;
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                                                                                                                                                                                                                    2436 TATTAACTITITITITITITITITITITITAGACAGTCTTTCTCTGTCACCCCAGGCTAGAG 2377
                                                                                                                                                                                      112 LILLILLILLILLILLILLILLILGGGAGAGLCLGCICGCCCAGGCLGGGG 171
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                                                                                                                                                                         gtanttttagtagagagggggtttcaccatgttgtccaggctggtctngaactcctgac 332
                                                                                     172 tacaatggtcggatcttggctcactgcaacctctgcctcccaggttcaagcaattcttct 231
                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;
                     19; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                            Human immune/haematopoietic antigen genomic sequence SEQ ID NO:20393.
                                                                                                                                             2376 TGCAGTAGCGTAATCTCGGCTCACACTCTGCCTCCCGGATTCAAGCAATTCTTCT
                                                                                                                                 ----ccaccacgcccagctaattttt
Length 9519;
                      34; Indels
  DB 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                               cytostatic; gene therapy; vaccine; metastasis; ds
 Score 206.8; DB 2
Pred, No. 4.1e-27;
0; Mismatches 34
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   17.4%;
82.8%;
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            Similarity 82.8
5; Conservative
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16-MAR-2000;
18-MAR-2000;
19-MAY-2000;
19-MAY-2000;
28-JUN-2000;
30-JUN-2000;
30-JUL-2000;
11-JUL-2000;
11-JUL-2000;
14-JUL-2000;
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24-FEB-2000;
              Best Local Sim
Matches 255;
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12-SEP-2000;
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 Human; reproductive system related antigen; reproductive system disorder;
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                                                                                                                            tacaatggtcggatettggctcactgcaacctctgcctcccaggttcaagcaattcttct 231
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                                  Gaps
                 17.4%; Score 206.8; DB 22; Length 56632;
82.8%; Pred. No. 4.3e-27;
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2000US-0198123.
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                                  Conservative
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          dational and a puryper of the binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful in medical disorders involving aberrant protein expression or biological activity. The polypeptide and polymucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. AAS64197-AAS94564 represent novel human diagnostic coding sequences of the invention.

Whote: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO
a polypeptide in tissue, as molecular weight markers and as
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Nucleic acids encoding human immune/hematopoietic antigen polypeptides, useful for preventing, diagnosing and/or treating cancers and metastasis -Ruben SM; Barash SC, WPI; 2001-483426/52. Rosen CA,

Disclosure; SEQ ID NO 28083; 3071pp + Sequence Listing; English.

AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I) amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic

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Ruben SM;
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Nucleic acids encoding human immune/hematopoietic antigen polypeptides,

PT useful for preventing, diagnosing and/or treating cancers and

PT useful for preventing, diagnosing and/or treating cancers and

PT metastasis -

NX

NX

ANX54951 to AAX64702 encode the human immune/haematopoietic antigen (1)

CC activity, and can be used in gene therapy and vaccine production. (I)

CC activity, and can be used in gene therapy and vaccine production. (I)

CC cample, they may be used in gene therapy and vaccine production. (I)

CC example, they may be used to treat disorders associated with decreased

CC example, they may be used to treat disorders associated with decreased

CC example, they may be used to produce a patient's genome

CC example, they may be used to treat disorders associated with decreased

CC example, they may be used to treat disorders associated with decreased

CC example, they may be used to treat disorders associated with decreased

CC supplement the patients own production of (1). Additionally, (1)

CC supplement the patients own production of (1). Additionally, (1)

CC polynucleotides may be used to produce the secreted (1), by Inserting

CC protein. (1) proteins and polynucleotides may be used to prevent,

CC diagnose and treat immune/haematopoietic-derived cells. AAX64703

CC cancers and cancer metastases of haematopoietic-derived cells. AAX64703

CC cancers and cancer metastases of haematopoietic-derived cells. AAX64703

CC cancers and cancer metastases of haematopoietic antigen genomic

CC ceancers and cancer metastases of haematopoietic antigen genomic

CC ceancers and cancer metastases of haematopoietic antigen genomic

CC sequences from the present invention. AAX64921 to AAX64950 and AAX64703

CC represent sequences used in the exemplification of the present invention.

X Sequence 37449 BP; 11842 A; 7890 C; 7531 G; 10186 T; 0 other;
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                                                                                                                                                          23253 AAAAAAGAAGTGTAATAAAGCTTCATAGATTTATCATCCAGACTAAATTATCAGTATTT 23194
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                                                                                      23193 ACCAMGITITITITITITITITITAGAGAGICICGCICTGICGCCCAGGCIAGAGIGCAG 23134
                                                                                                                                                                                                                                                                          23133 TGGCATGATCTCGGCTCACTGCAAGCTCCACCTCCCAGGTTCAAGCGATCTCCCTGCCTC 23074
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                                                             1 gatogogocactgoactocagoctgggtgagagagagagactctgtctoaaaaaaaaa 60
                                26; Gaps
Score 204.2; DB 22; Length 37449;
                              80; Indels
              Pred. No. 1.2e-26;
0; Mismatches 80
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74.9%;
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Matches 317; Conservative
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AAK68202 standard; DNA; 56743 BP.

RESULT 11

AAK68202

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I) amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic activity, and can be used in gene therapy and vaccine production. (I) proteins and polynucleotides may be used in the prevention, diagnosis and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           proteins and polymucherotuses may be used in the prevention of diseases associated with inappropriate (I) expression. For example, they may be used to treat disorders associated with decreased expression by rectifying mutations or deletions in a patient's genome that affect the activity of (I) by expressing inactive proteins or to supplement the patients own production of (I). Additionally, (I) polynucleotides may be used to produce the secreted (I), by inserting the nucleic acids into a host cell and culturing the cell, by inserting protein. (I) proteins and polynucleotides may be used to prevent, diagnose and treat immune/haematopoietic-related diseases, especially cancers and cancer metastases of hematapoietic-derived cells. AAK64703 to AAK87694 represent human immune/haematopoietic antigen genomic sequences from the present invention. AAK87492 to AAK874950 and AAM82169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           represent sequences used in the exemplification of the present invention.
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08-DEC-2000; 2000US-0251990.
11-DEC-2000; 2000US-0254097.
05-JAN-2001; 2001US-0259678.
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Human immune/haematopoietic antigen genomic sequence SEQ ID NO:36572.
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AAK81760 standard; DNA; 56743 BP.
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                Human; immune; haematopoietic; immune/haematopoietic antigen; cancer; cytostatic; gene therapy; vaccine; metastasis; ds.
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                                                                                          2249 aagtatccttttaataacttggaataaag 2277
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and a ARK64951 to a AK64702 encode the human immune/haematopoietic antigen (1) and acid sequences given in AAM82170 to AAM91921. (1) have cytostatic activity, and can be used in gene therapy and vaccine production. (I) proteins and polynucleotides may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate (1) expression. For example, they may be used to treat disorders associated with decreased expression by rectifying mutations or deletions in a patient's genome that affect the activity of mutations or deletions in a patient's genome cuplement the patients own production of (1). Additionally, (1) polynuclectides may be used to produce the secreted (1), by inserting the nucleic acids into a host cell and culturing the cell to express the protein. (I) proteins and polynuclectides may be used to prevent, diagnose and treat immune/haematopoietic-related diseases, especially cancers and cancer metastases of haematopoietic arityed cells. AAK64703 cancers and cancer metastases of haematopoietic arityed genomic sequences from the present invention. AAK54942 to AAK54950 and AAM82169 represent sequences used in the exemplification of the present invention.
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5210 TCCTGCCTCAGCCTCCCAAGTAGCTGGGATTATAGGCCCCTGCCACCACGCCCAGCTAAT 5151

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Job time: 12455 sec

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Ruben SM;
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                   2000US-0249218
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                                                                                                                                                                                                                                            The invention relates to movel genes (ABA11004-ABA21534) and proteins (ABB14678-ABB18001) useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. The genes are isolated from a range of human lissues disclosed in the specification. The nucleic acids, proteins, antibodies and (ant)agonists are useful in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mucleic acids encoding 3224 human nervous system antigen polypeptides,
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                                                  diagnosing and/or treating nervous system
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                                                                                                                                                                Disclosure; SEQ ID NO 8929; 1701pp + Sequence Listing; English,
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0; Mismatches
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Matches 259; Conservative
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Homo sapien 7 Homo sapi

Sequence

AC020697 F AX348476 SAR103889 S X02308

AX330682 Sequence AX330906 Sequence AX335755 Sequence

76 Sequence 89 Sequence Human mRNA 91 Sequence

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HUMIS 1186 bp DNA linear PRI 06-NOV-2001
Homo sapiens gene for thymidylate synthase, exon 1, partial cds.
D00517
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BC012567 Homo sapi
BC005793 Homo sapi
AC005703 Homo sapi
AL357374 Human DNA
AL357374 Human DNA
AL355984 Human DNA
AC016907 Homo sapi
AC0163526 Human Chro
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AC038991 Homo sapi
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Human thymidylate synthase gene: isolation of phage clones which cover a functionally active gene and structural analysis of the region upstream from the translation initiation codon 3. Biochem. 106 (4), 575-583 (1989)
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Takeishi, K., Kaneda, S., Ayusawa, D., Shimizu, K., Gotoh, O. and
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University of Shizuoka School of Food and Nutritional Sciences 395

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MGLGVPFNIASYALLITMLAHITGLKPGDFIHTLGDAHIYLNHIEPLKIQLQREPRP
PRIAILINYEKIDDFKAEDFQIEGYNPHPIKMEMAV"
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Pred. No. 3e-191;
0; Mismatches 10; Indels
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//note="11 sequence"
10125. .10389
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12567. .12743
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12807. .13084
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13449. .13624
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16228. .16233
17262. .17553
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13625. .14132
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Best Local Similarity 99.1%;
Matches 1176; Conservative
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3049. 3347
/note="Alu s
4953. 5245
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1660. .16
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FERTURES Location/Qualifiers source 11186 /organism="synthetic construct" //db_xref="taxon:32630" /note="chemically treated genomic DNA (Homo sapiens)" DASE COUNT 229 a 98 c 386 g 473 t ORIGIN	Query Match 64.7%; Score 767.4; DB 6; Length 1186; Best Local Similarity 78.4%; Pred. No. 6.2e-123; Matches 926; Conservative 0; Mismatches 254; Indels 1; Gaps	Oy 2 atogogocactgoactcoagoctgggtgagagagogagactctgtctcaaaaaaaaa 61	Qy 62 aaaagaccgccaggctcaaacaaaaacctcggaaaagccctggcggtctttttttt	Qy 122 tttttttttttttttttgggacagtcttgctctgtcgcccaggctggagtacaatggtc 181	Qy 182 ggatottggctcactgcaacctctgcctccaggttcaagcaattcttctgcctcagcct 241	Qy 242 cccaagtagccaccacgcccagctaattttgtanttttagtagaagggggtttcacc 301	QY 302 atgitgiccaggetggictngaactectgaccteaggtgatecacegecteggeeeecc 361	Oy 362 aaagtactaggattacaggcgtgagccaccgcgtccagcgccctggcggtttttaatcaa 421	Oy 422 gtagaaagctgcattataccacttgcttcngttgcnttcagtgagaacgaagaaatgga 481 	Oy 482 aatgcaaatAncttattagttgtaggaaacagatctcaaacagcagttttgtngacaaga 541	Oy 542 ocgoaggaaacgtgggaactgtgctgctggcttagagaaggcgcggtcgaccagacggt 601	Oy 602 toccaaagggcgcagtcettcccngccaccgcacctgcntccaggttcccgggtntccta 661	Oy 662 agactctcagctgtgggcctgggctccgttctgtgccacacccgtggctcctgcgtttcc 721	Oy 722 ccctggcgcacgctctctagagcggggccgcgcgcgcgcg	Qy 782 agogoggacgogggaaaaggogogoggaagggtcctgccacogogccacttggc 841	QY 842 ctgoctccgtcccgccacttggcctgctccgtccgccgcgcacttcgcctgc 901
391 cgcgtccagcgccctggcggtttttaatcaagtagaaaagctgcattataccacttgctt 450	Cagatotoaaacagcagttttgtngacaagaccgcaggaaacgtgggaactgtgctct	571 ggcttagagaaggcgcggtcgaccagacggttcccaaagggcgcagtccttccngccac 630	631 ogcaectgentecaggttcecgggtntectaagactetcagetgtggeectgggeteegt 690	691 tctgtgccacacccgtggctcctgcgtttcccctggcgcacgctctctagagcgggggc 750	751 cgccgcgacccgccgagcaggaagaggcggagcggggacggcgg	9 811 oggaaggggtoctgccaccgcgccacttggcctgcctccgtcccgcgcgcacttggc 870	7 871 tgcctccgtccgccgcgccacttcgcctgcctccgccgccgccgccgccatgcct 930	y 931 gtggccggctcggagctgccgcgcgcccCtgcccccgccgcacaggagcggacgc 990	y 991 gagccgcgtccgccgcacggggagctgcagtacctggggcagatccaacatcctccgc 1050 	Y 1051 tgcggcgtcaggaaggacgaccgcacgggcaccctgtcggtattcggcatgcag 1110 	y 1111 gccgctacagcctgagaggtgacgccgcgggcccctgcgggacgggacggggaaggag 1170	y 1171 ggaggogggtgggga 1187 	9 777	UCUS DIAS DNA 11near FAT 06-FEB-2002 EEFINITION ASSUBATO EESTION AX348477 GI:18614513	synd synd art:	AUTHORS 1 (91-0-7). Piepenbrock, C. and Berlin, K. AUTHORS Method and nucleic acids for pharmacogenomic methylation analysis JOURNAL Patent: WO 0202806-A 172 10-JAN-2002; Epigenomics AG (DE)

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                                                                                                                                                                  74 Trgccreccreccrecceccecceccecceccecces 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nucleotide sequence of a functional cDNA for human thymidylate
                                                                                                                                                       893 ttcgcctgcctccgtccccgccgccgccatgcctgtggccggctcggagctgccgc 952
                                                                                     Gaps
                                                                                                                       14 CCACTIGGCCTGCCTCCGTCCGCCGCGCCACTTGGCCTGCCTCCGCCCCGCGCCAC 73
                                                                                                                                                                                                             134 GCGGCCCTTGCCCCCCGCCGCACAGAGCGGGACGCCGAGCCGCGTCCGCCGCACAGAGGGGGG
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                                                               Length 1536;
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                                                                                     Indels
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1. 1536
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85215597
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                                                               DB 6;
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//note="pot. stem-loop structure"
35. .103
/note="pot. stem-loop structure"
                                                               Score 297.8; DB 6 Pred. No. 4.3e-42;
                                                                                     0; Mismatches
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                   378
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369 c 399 g
                                                               25.1%;
99.3%;
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                                                                                     Matches 299; Conservative
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/translation="mpVMGSELPRRPLPPAAQERDAEPRPPHGELQYLGQIQHILRCG
VRKDDRTGTGTLSVFGWQARYSLRDEFPLLTTRRVFWRGTLEELLWFTKGSTRAKELS
SKGYKIWDANGSRDFLDSLGFSTREEGDLGFVRGYRGWRHGTLEELLWFTKGSTRAKELS
LGRVIDTITTRTWDDRRIIMCAWNPRDLPLMALPPCHALQFTVWSELSCQIYGRSGW
MGLGYPFNTARSPLLTYMATAHITGLKFGDFTHTLGDAHITINHIEPLKIQLQREPRPF
PKLRILRKVEKIDDFRAEDFQIEGYNPHPTIKMEMAV"
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Shiffman, D., Somogyi, R., Lawn, R., Seilhamer, J.J., Porter, G.J.,
Mikita, T. and Tai, J.
Genes expressed in foam cell differentiation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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/note="pot. polyadenylation signal"
1519. .1524
/note="pot. polyadenylation signal"
1536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 297.8; DB 9;
Pred. No. 4.3e-42;
0; Mismatches 2;
/note="pot. stem-loop structure" 70. .72
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                                                                                                                                                                                                                                                                                                                                                                                                                     /note="polyadenylation site"
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106. .1047
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104. .106
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Sequence 200 from Patent WO0177389.
                          /note="direct repeat 1" 97. .103
                                                                                                                                                              /codon_start=î
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cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: National Institutes of Health Intramural
Sequencing Center (NISC),
Gaithersburg, Maryland;
Web site:

nisc_mgc@nhgri.nih.gov
Contact:
nisc_mgc@nhgri.nih.gov
Shevchenko,Y., Wetherby,K.D., Beckstron-Sternberg,S.M.,
Benjamin,B., Blakesley,R.W., Bouffard,G.G., Brinkley,C., Brooks,S.,
Dietrich,N.L., Guan,X., Gupta,J., Ho,S.-L., Karlins,E., Legaspi,R.,
Lim,M., Maduro,Q.L., Masiello,C., Mastrian,S.D., McCloskey,J.C.,
McDowell,J., Pearson,R., Snyder,B., Stantripop,S., Thomas,P.J.,
Tiongson,B.E., Touchman,J.W., Tsurgeon,C., Vogt,J.L., Walker,M.A.,
Zhang,L.-H. and Green,E.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LiAL at: http://image.llnl.gov Series: IRAL Plate: 4 Row. p Column: 19
fais clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 4507750.
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MGLQVPRNIASYALLITVMIAHITGLRQDFIHTIGDAHIYLNHIEPLKIQLQREPRPF
PKLRILRKVBKIDDREDPQIEGYNPHPTIKMEMAV"
PKLRILRKVBKIDDRG
389 G 389 G 376 t
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/clone_lib="NIH_MGC_21"
/lab_host="DH10B-R"
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/organism="Homo sapiens"
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/db_xref="taxon:9606"
/clone="MGC:1590 IMAGE:3138877"
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Search completed: July 26, 2002, 16:39:18 Job time: 24232 sec Sequence Sequence (Sequence 4 Sequence 3 Sequence 3 Appl Appl

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US-09-089-195-1
; Sequence 1, Application US/09089195
; Sequence 1, Replication US/09089195
; Patent No. 6087489
; Patent No. 6087489
; TITLE OF INVENTION: APPLICANT: APPLICANT
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Nuclectina thymidylate synthase
Nucleic Acids Res.
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            US-08-483-533-18
US-09-283-471A-18
US-09-165-533-4
US-09-165-283-4
US-09-165-264-13
US-09-165-264-13
US-09-283-471A-38
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US-07-945-283-1
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US-08-093-453B-1
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APPLICATION NUMBER: US/09/089,195
FILING DATE: herewith
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WRDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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REFERENCE/DOCKET NUMBER: ISPH-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (609) 810-1454
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1536 Dase pairs
TYPE: NUCleic Acid
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PUBLICATION INFORMATION:
AUTHORS: Takelshi, K.
AUTHORS: Kaneda,S.
AUTHORS: Avusaum
CORRESPONDENCE ADDRESS:
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Ayusawa,D.
Shimizu,K.
Gotoh,O.
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                       GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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4 US-08-406-030A-3

2 US-08-609-443B-17

4 US-09-165-264-7

4 US-09-165-264-7

4 US-09-283-471A-39

4 US-09-283-471A-39

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5 US-08-804-27C-7
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                                                                                                                                                                                                                                                                                                                                                                 383533 seqs, 122816752 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                                                      nucleic search, using sw model
                                                                                                                                                                                                                                                                                                       IDENTITY_NUC Gapor 10.0 , Gapext 1.0
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US-08-770-379-17/c
       Best Local Sim
Matches 592;
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APPLICANT: Nicholas, John
APPLICANT: Nicholas, John
APPLICANT: Reitz, Marvin
TITLE OF INVENTION: No. 6264958el Genes of Kap
TITLE OF INVENTION: No. 6264958el Genes of Kap
TITLE OF INVENTION: Associated Herpesvirus
TITLE OF INVENTION: No. 6264958el Genes of Kap
TITLE OF INVENTION: NO. 6264958el Genes of Kap
TITLE OF INVENTION: 1107, 78372
CURRENT APPLICATION NUMBER: 1999-11-23
CURRENT FILING DATE: 1999-11-23
PRIOR FILING DATE: 1996-07-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION NUMBER: PCT US 97/12931
PRIOR FILLING DATE: 1997-07-24
NUMBER OF SEQ ID NOS: 62
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Patent No. 6264958
GENERAL INFORMATION:
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LENGTH: 1014
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US-09-230-637-1
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Score 387.4; DB 4
Pred. No. 1.8e-93;
0; Mismatches 341
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                                                                                                                                                     Length 35100,
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                                                                                                                                                  Score 387.4; DB 4;
Pred. No. 1.1e-92;
0; Mismatches 341;
TELEFAX: (212) 391-0525
; INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
: LENGTH: 351.00 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: double
: TOPOLOGY: linear
: MOLECULE TYPE: DNA (genomic)
US-08-757-669A-17
                                                                                                                                                    Match 25.2%;
Local Similarity 63.5%;
Hes 592; Conservative
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GENERAL INFORMATION:
APPLICANT: Chang, Yuan
APPLICANT: Boheraky, Roy A
APPLICANT: Beleave, James J
APPLICANT: Edelman, Isidore S
APPLICANT: Moore, Patrick S
APPLICANT: Moore, Patrick S
APPLICANT: Moste, Moste, Patrick S
APPLICANT: Moste, Moste, Patrick S
APPLICANT: Moste, Mo
20183 ICIGITICITCCAIGGAAGAGTTTACACCTGAIGATTTAGACTGGIGGACTACTGCCCG 20124
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Pred. No. 1.1e-92;
0; Mismatches 341; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; TYPE: DNA
; ORGANISM: Kaposi's sarcoma-associated herpesvirus
US-09-230-371A-17
                                                                                                                                                                                                       20123 CATCCTACCATTCGTATGGAAATGGCAGTATAG 20091
                                                                                                                    catccaactattaaaatggaaatggctgtttag 1047
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/09/230,371A CURRENT FILING DATE: 1999-11-17 PRIOR APPLICATION NUMBER: PCT/US97/13346 PRIOR FILING DATE: 1997-07-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; Sequence 17, Application US/09230371A; Patent No. 6348586
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          25.2%;
63.5%;
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SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches 592; Conservative
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                              RESULT 6
US-09-230-371A-17/c
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APPLICANT: Schmid, Molly B.
APPLICANT: Sun, Dongxu
TITLE OF INVENTION: METHODS OF SCREENING FOR COMPOUNDS
TITLE OF INVENTION: ACTIVE ON STAPHYLOCOCCUS AUREUS
NUMBER OF SEQUENCES: 111
                                                                                                                                                                                                                                                                                                                                                                                                          SUFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/265,315
FILING DATE: March 9, 1999
CLASSIFICATION: 435
PATCR APPLICATION: 435
                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT RECREATED:

ATTORNEY/AGENT RECREATION:

NAME: Warburg, Richard J.

REGISTRATION NUMBER: 32.427

TERFORM
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APPLICATION NUMBER: 08/714,918
FILING DATE: September 13, 1996
APPLICATION NUMBER: 60/009,102
FILING DATE: December 22, 1995
                                                                                                                                                                                                                  E: Lyon & Lyon
633 West Fifth Street
Suite 4700
            Lee, Ving J.
Malouin, Francois
Martin, Patrick K.
Schmid, Molly B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: 24
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (213) 489-1600
Benton, Bret
                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                               Los Angeles
California
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90071-2066
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                                                                                                                                                                                                                  ADDRESSEE:
STREET: 63
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US-09-265-315-7
                                                                                                                                                                                                                                                                             CITY: LOS
STATE: CR
COUNTRY:
                                   APPLICANT:
                                                        APPLICANT:
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Pred. No. 1.7e-22;
6; Mismatches 194;
                SYSTEM: IBM P.C. DOS 5.0 Word Perfect 5.1
                                                                                                              CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/714,918
FILING DATE: September 13, 1996
APPLICATION NUMBER: 60/009,102
FILING DATE: December 22, 1995
APPLICATION NUMBER: 60/003,798
FILING DATE: September 15, 1995
ATTORNEY/AGENT INFORMATION:
                                                                             US/09/265,315
                                                                                                                                                                                                                                                                                                                                            240/247
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US-09-265-315-7/c
; Sequence 7, Application US/09265315
; Partent No. 6187541
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                               TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-5510
INPORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 3479 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                    NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 24(
TELECOMMUNICATION:
                                                                             APPLICATION NUMBER: US/09/:
FILING DATE: March 9, 1999
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  IBM Compatible
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Matches 268; Conservative
                                                        CURRENT APPLICATION DATA:
                    OPERATING SYSTEM:
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US-09-265-315-7
                                                                                                FILING DATE:
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                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                     4;
                                                                                                                                                                                                                                                                                                DB 4; Length 3479;
                                                                                                                                                                                                                                                                                             Query Match 7.9%; Score 121.2; DB 4; Length Best Local Similarity 56.8%; Pred. No. 1.7e-22; Matches 268; Conservative 6; Mismatches 194; Indels
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 34'9 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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FILING DATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        130 ccgcgcccttgccccccgccgcacaggagcgggacgccgagggcgcgcgcgcac 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                413 GCGCGCCTGCGCCTGCGACGCGCGGGGGGGGGGGCGCCGGAGCCCCCCCGGGACCCCC 472
                                                                                                                                                                                                                                                                                                                                                                                                     0; Gaps
                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Roizman, Bernard
APPLICANT: Chou, Joany
TITLE OF INVENTION: Method For Treating Tumorigenic Diseases
                                                                                                                                                                                                                                                                                3.2%; Score 48.6; DB 4; Length 503; 54.1%; Pred. No. 0.0012;
tive 0; Mismatches 84; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           E: Marshall, O'Toole, Gerstein, Murray & Borun 6300 Sears Tower, 233 South Wacker Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
PAPLICATION NUMBER: US/09/283,471A
FILING DATE: 04-APR-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Zeller, James P.
REGISTRATION NUMBER: 28,491
REFERENCE/DOCKET NUMBER: 27373/32742A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RY: United States of America 60606-6402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; Sequence 7, Application US/09283471A; Patent No. 6340673; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: 07/861,233
APPLICATION NUMBER: 07/861,233
FILING DATE: 31-MAR.1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/419,853
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    08/483,533
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                MOLECULE TYPE: DNA (genomic)
                                   TELERX: 312/474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 7:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
                    TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 11-APR-1995
                                                                                       SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
LENGTH: 503 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                              Best Local Similarity 54.19
Matches 99; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: 514
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES: 4. CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
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STREET: BOLL
CITY: Chicago
                                                                                                                                                                                 linear
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70 ceacttegectgecteegteecegeeegeegegegeatgeetgtggeeggeteggagetg 129
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                                                                                                                                                                                                                                                                                                                                                                                                         0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       293 GEGCCCCCACCECCCGGCGTGGGCCCGGGGGCGGGCTGACCCCTCCCACCCCCTCG 352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         353 caccerrecacerrecaceaceacecerecacerecacerecacerecaceaceaceae 412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           130 ccgcgccggcccttgcccccgccgcacaggagcgggacgccgagccgcgtccgccgcac 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                           10 gggaccaettggcetgcetecgtecegeegeegeettggeetgeetecgteegeege 69
                                                                                                                                                                                                                                                                                                                                                    Query Match 3.2%; Score 48.6; DB 4; Length 503; Best Local Similarity 54.1%; Pred. No. 0.0012; Matches 99; Conservative 0; Mismatches 84; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5: Marshall, O'Toole, Gerstein, Murray & Borun
6300 Sears Tower, 233 South Wacker Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Roizman, Bernard
APPLICANT: Chou, Joany
TITLE OF INVENTION: Method for Treating Tumorigenic
NUMBER OF SEQUENCES: 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: PatentIn Release #1.0, Version #1.25
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07-MAR-95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 37, Application US/08483533
Patent No. 6172047
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION DATA:
PRIOR APPLICATION DATA:
08/419,853
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           07/861,233
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               28,491
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                                                                                                                                                                                                                                                  MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                   LENGTH: 503 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 11-APR-95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                             linear
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Illinois
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ZIP: 60606-6402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION:
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0;
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                                                                                                                                                                                                                           0; Gaps
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TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

HYPOTHETICAL: NO

ANII-SENSE: NO

ORIGINAL SOURCE:

CREANISM: Herpes simplex virus

STRAIN: Herpes Simplex virus

FEAUTHE:

RAME/KEY: CDS

LOCATION: 1..702

US-08-458-568A-3
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Search completed: July 26, 2002, 17:46:36 Job time: 12445 sec

Sequence 7, Application US/09963333
GENERAL INFORMATION:
APPLICANT: Stanton, Jr., Vincent P.
TITLE OF INVENTION: THYMIDINE SYNTHASE GENE SEQUENCE VARIANCES
TITLE OF INVENTION: EAVING UTILITY IN DETERMINING THE TREATMENT
TITLE OF INVENTION: OF DISEASE
FILE REFERENCE: 11926-015002

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APPLICANT: Stanton, Jr., Vincent P.
TITLE OF INVENTION: THYMIDINE SYNTHASE GENE SEQUENCE VARIANCES
TITLE OF INVENTION: HAVING UTILITY IN DETERMINING THE TREATMENT
FITLE OF INVENTION: OF DISEASE
FILE REFERENCE: 11926-015002
                                                                                                                                                                                                                 PRIOR PELLING DATE: 2001.09.656,659
PRIOR FILING DATE: 2000-09-08
PRIOR APPLICATION NUMBER: 09/596,033
PRIOR APPLICATION NUMBER: 09/596,033
PRIOR FILING DATE: 2000-06-15
PRIOR PELLING DATE: 1999-07-20
PRIOR FILING DATE: 1999-07-20
PRIOR PILING DATE: 1999-07-19
PRIOR FILING DATE: 1999-07-19
PRIOR PILING DATE: 1998-07-19
PRIOR PILING DATE: 1988-07-20
NUMBER OF SEQ ID NOS: 16
SOFWARE: Fast-SEQ for Windows Version 4.0
SEQUENTIOR OF SET DATE: 1988-07-20
                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/09/963,333 CURRENT FILING DATE: 2001-09-24
Sequence 6, Application US/09963333 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LOCATION: 1066
OTHER INFORMATION: n = t or c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: misc_feature
LOCATION: 1136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURE:
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FILE MEMBERS. ELSCOULOS.
CURRENT APPLICATION NUMBER: US/O9/963,333
CURRENT PILING DATE: 2001-09-24
PRIOR APPLICATION NUMBER: 09/68,659
PRIOR FILING DATE: 2000-09-08
PRIOR FILING DATE: 2000-06-15
PRIOR FILING DATE: 1200-06-15
PRIOR FILING DATE: 1999-07-20
PRIOR FILING DATE: 1999-07-20
PRIOR PRILING DATE: 1999-07-20
PRIOR PILING DATE: 1999-07-20
PRIOR FILING DATE: 1999-07-19
PRIOR FILING DATE: 1999-07-19
PRIOR FILING DATE: 1998-07-20
NUMBER: PRIOR FILING DATE: 1998-07-20
NUMBER: PRIOR FILING DATE: 1998-07-19
SOFWWARE: FRACESQ for Windows Version 4.0

ggačajtettgetetgtegeceageetggafactacaatgjeeggatettggeteaetgeaectetgeete ecaggiteaageaattettetgeeteageeteecaagtageeaecaegeceagetaattittgianitit agtagaacgggggtttcaccatgttgtccaggctggtctngaactcctgacctcaggtgatccacccgc ctogoccoccómagotactaggattacaggogigagocacogogtocagogocotggogotttttaatca agtagaaaagotgoattataccacttgottcngttgonttcagtgagaaagaaatggaaatggaaat Ancttattagttgtaggaaacagatotcaaaacagcagttttgingacaagaccgcaggaaaacgtgggaa ctytyctycigittägagaagýcycygtcyacčagácygttccčaaagýgcycattccčnococ cycacctycntccayyttcccygytntcctaagactctcayctytygccctygyctccyttctytycac accogtogotectgogitticcoccitogogoacgeitetetagagogogogogocgeogogacecgoogagoa cetgeeteegteeegeegeeacttggeetgeeteegteegeegegegegegettegeetgeeteegtee cegecegeegegatatetgtggceggeteggagetgeegegeeggeeegtgeeectgeegeagga gegggaegeegageegegteegeegeaegggggagetgeagtaeetgggggaagateeaacacateege tgeggegteaggaaggaegaeegeaegggeaeegggeaeeetgteggtafteggeatgeaggegegetaea

gócagttetatytýgtgaacagtgagctytectgecagetgtaecagagategygagaeatgygectegy tytgecttteaacategoecagetaegecetycteaegtaegtgettgegaacateacaggectgaageca gytgaetttatacacactttyggagtatgeacatatttaettgaateaeactegagecatgaaaattaage tteagogagaacecagacettteecaaageteaagattetteectgaataaaattgaagatteaea

tttgotctaaaaagaaGaaggaactaggtcaaaaatotgtccgtgacotatcagttattaatttttaagga tgttgccactggcaaatgtaactgtgccagttctttccataataaaaggctttgagttaactcactgagg

gotttoaaaggagotCgaaaggatattgtcagtotttaggggttgggotggatgccgaggtaaaagttott

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tatqtqcatttcaatcccacqtacttataaaqqaaqqttqqtqaatttcacaaqctatttttqgqaatattt

agaatcatcatgtgcgcttggaatccaagagatcttcctctgatggcgctgcctccatgccatgcctct

teggeatgeaggegegetacageetgagagatgaatteeetetgetgacaaceaaaegtgtgttetggaa gggtgttttggaggagttgctgtggtttatcaagggatccacaaatgctaaagagctgtcttccaagggga gtgaaatctgggatgccaatggatcccgagactttttggacagcctgggattctccaccagagaagaag

cagateceaacacatectecegetgeggegteaggaaggaegaecgeaeegggeaeeggeaeeetgteggta

OTHER INFORMATION: nucleotide in position 458 is c, or absent

OTHER INFORMATION: n = c or a

LOCATION: 458

OTHER INFORMATION: n = a NAME/KEY: misc_feature LOCATION: 452, 640

NAME/KEY: misc_feature LOCATION: 492, 625 NAME/KEY: misc_feature

LOCATION: 276, 321, 534, 656 OTHER INFORMATION: n = c or

TYPE: DNA ORGANISM: Homo sapiens NAME/KEY: misc_feature

FEATURE:

LENGTH: 1187

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July 26, 2002, 14:31:46 ; Search time 406.4 Seconds
(without alignments)
6489.125 Million cell updates/sec
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SIDSI/gcgdata/genesequ/genesequ-embl/NA1981. DAT:*
SIDSI/gcgdata/geneseqy/genesequ-embl/NA1983. DAT:*
SIDSI/gcgdata/geneseqy/genesequ-embl/NA1983. DAT:*
SIDSI/gcgdata/geneseqy/genesequ-embl/NA1986. DAT:*
SIDSI/gcgdata/geneseqy/genesequ-embl/NA1986. DAT:*
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1736436 segs, 858457221 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                  OM nucleic - nucleic search, using sw model
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Maximum DB seq length: 200000000
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1536
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                                                                                                                                                                                                                                                                                                                                                                                                          Sequence:
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                                                                                                                                                                                                   Run on:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	Human DNA sequence	DNA encoding novel	Thymidylate syntha	Human thymidylate	Human thymidylate	Nucleotide sequenc	Nucleotide sequenc	Macaca mulatta rha	Human herpesvirus
	AAS94945	AS84960	AAF31109	1091215	4X24270	AAH74201	MT4202	3C64754	4V10240
A		23 AZ	22 A		-	22 A		21 A	9 A
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Lengt		1539	1859	18596	26	26.6 124884	12515	13371	101
% Query Match Length DB	97.3	83.4	39.9	39.8	32.6	26.6	26.6	26.3	25.2
Score	1494.8	1281.4	613.2	613.2	501.2	408	408	404.6	387.4
sult No.	~	~	m	4	Ŋ	9	7	ω	σ
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AAV73802	1 1	1 - 1	315	0 8 8	680	276	892	574	19	398	354	158	AAS04572	151	+1	AAA81489	AAH81382	789		341				AAH65907	AAF72247	AAH68526	AAX60894	AAS84962	AAA26856	AAS08007	AAF91538	9	952	AAV43438
70	4 6	9 6	2 2	23	20	22	22	23	23	22	22	22	22	21	21	21	22	23	23	23	18	23	18	22	22	22	20	23	21	22	22	19	23	13
35100	7	1	346	346	1839	870	305107		651	1857	96109	196	196	35133	349980	(*)	795	1068	1328	1323	580073		5924	798	798	349980	9603	2945	3479	3479	3479	118	26879	861
25.2	20.0	24.0	24.7	1.00	21.7	20.0	20.0	19.4	15.2	14.4	12.9	12.3	12.0	11.9	11.9	11.9	11.7	11.7	11.0	10.1	9.	8	8	8,3	8,3	8	8.1	7.9	7.9	7.9	7.9	7.7	7.3	6.3
387.4	00000	000	277.0	330.0	333.4	307.6	307 6	298.2	233.2	221.6	197.6	188.8	184.8	183.2	183.2	183.2	180	ത	168.2	-	5	32	131.6	26	26	26	24	121.6	23	2	2	17	112	96
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ALIGNMENTS

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AAS94945 standard; DNA; 3298

AAS94945 ID AAS94

RESULT

AAS94945;

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Mikita T;
                                      Human DNA sequence #200 expressed during foam cell differentiation.
                                                        Human; foam cell differentiation; atherosclerosis; cerebral stroke; cardiovascular disorder; coronary artery disease; gene therapy; ds.
                                                                                                                                                                                               Porter GJ,
                                                                                                                                                                                               Seilhamer JJ,
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                                                                                                                                                                                                 Lawn
                                                                                                                                                                              (INCY-) INCYTE GENOMICS INC.
                                                                                                                                          04-APR-2001; 2001WO-US11128.
                                                                                                                                                           05-APR-2000; 2000US-195106P
                         (first entry)
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                                                                                                                                                                                                Shiffman D, Somogyi
                                                                                                                                                                                                                            WPI; 2002-010925/01
                                                                                                       WO200177389-A2.
                        14-FEB-2002
                                                                                       Homo sapiens.
                                                                                                                         18-OCT-2001.
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Composition useful for diagnosis of conditions, disorders or diseases associated with atherosclerosis, comprises several polynucleotides that

1239 CTGTCTTCCAAGGGAGTGAAAATCTGGGATGCCAATGGATCCCGAGACTTTTTGGACAGC 1180

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome polymerase chain recombinant production of (II). The collection are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques for restore normal activity of (II) at useful in gene therapy techniques (II). (II) is useful for generating antibodies against it, detecting or quantitating a polymeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and diagnostic coding sequences. Assetting the products dependent on bNA and diagnostic coding sequences of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   printed
from WIPO
                                                                                                                                                                                                                                                                                                                           New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess biodiversity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Note: The sequence data for this patent did not appear in the specification, but was obtained in electronic format directly at ftp.wipo.int/pub/published_pct_sequences.
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                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1; SEQ ID No 20764; 103pp; English
                                                                                                                                                                                                                      Tang YT;
                                                                                                           2000US-0540217.
2000US-0649167.
                                                               30-MAR-2001; 2001WO-US08631
                                                                                                                                                                                                                                                             WPI; 2001-639362/73.
P-PSDB; ABG20773.
                                                                                                                                                                                                                      Drmanac RT, Liu C,
                                                                                                                                                                           (HYSE-) HYSEQ INC
                                                                                                           31-MAR-2000;
                                                                                                                               23-AUG-2000;
                      11-OCT-2001
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10; ATGCAGGCGCGCTACAGCCTGAGAGAGATTCCCTCTGCTGACAACCAAACGTGTGTTC 1300 TGGAAGGGTGTTTTGGAGGAGTTGCTGTGGTTTATCAAGGGATCCACAAATGCTAAAGAG 1240 CTCCGCTGCGGCGTCAGGAAGGACGACGCACGGGCACCGGCACCCTGTCGGTATTCGGC 1360 345 225 285 405 465 Gaps 166 gacgeegageegeteegeegeacggaggagetgeagtaeetgggggaagateeaacaate ctccgctgcggcgtcaggaaggacgacggcacgggaccggcacctgtcggtattcggc atgoaggogogotacagoctgagagatgaattccctctgctgacaaccaaacgtgtgttc tggaagggtgttttggaggagttgctgtggtttatcaagggatccacaaatgctaaagag ctgtcttccaagggagtgaaaatctgggatgccaatggatcccgagactttttggacagc Length 1539; 16; 21; Indels DB 23; Score 1281.4; Pred. No. 0; Pred. No. 0; 0; Mismatches Query Match 83.4%; Best Local Similarity 97.4%; Matches 1410; Conservative 1419 1359 1479 226 286 346 1299 406 ð 임 Q В QΣ 合 δy 임 QYq ó

1059 CTGCAAAGAGTGATTGACACCATCAAAACCAACCCTGACGACAAGAAGAATCATCATTTGC 1000 tgaagggtacaatccgcatccaactattaaaatggaaatggctgtttagggtgctttcaa 1058 gaatgaaatgtatgtgetettag-caaaaacatgtatgtgeattteaateceaegtaett 1356 1357 ataaagaa-ggttggtgaatttcacaagctatttttggaatattttagaatattttagaal 1415 aatttoacaagctattocotcaaatctgagggagotgagtaacacocatcgatcatgatgt 1475 ggetttgagttaaeteaetgagggtatetgaeaatgetgaggttatgaacaaagtgagga 1297 1476 agagtgtggttatgaactttaA----agttgttttatatgttgctataataagaagt 1529 940 939 gottoaggattottogaaaagttgagaaaattgatgacttoaaagotgaagactttoagat 998 219 AAITICACAAGCIATICCCTCAAATCIGAGGAGGTGAGTAACCCCATCGATCATGATGT 160 761 821 880 459 AATITITAAGGAIGGIIGCCACIGGCAAAIGIAACIGIGCCAGIICITICCAIAAIAAAA 400 466 ctgggattctccaccagagaagaagaaggggacttgggcccagtttatggcttccagtggagg 526 cattttggggcagaatacagagatatggaatcagattattcaggacagggagttgaccaa ctgcaaagagtgattgacaccatcaaaaccaaccctgacgacagaagaatcatgtgc gggcctcggtgtcctttcaacatcgccagctacgccctgctcacgtacatgattgcgca catcacgggc-ctgaagccaggtgactttatacacactttgggagatgcacatatttacc 881 tgaatcacatcgagccactgaaaattcagcttcagcgag--aacccagacctttcccaaa 579 AGGAGCTCGAAGGATATTGTCAGTCTTTAGGGGTTGGGCTGGATGCCGAGGTAAAAGTTC aatttttaaggat-gttgccactggcaaatgtaactgtgccagttctttccataataaa 1119 1416 666 1179 339 586 762 822 g g g qq δž QQ δŏ qq ŏ g Qγ g Qγ g QYg g QΫ q δŽ g δy QY g QYDp QΫ QVDp QYg δ 셤 $Q\underline{Y}$ δŽ δŽ

cytostatic;

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New antisense oligonucleotides directed against thymidylate synthase
                                                                                                                                                     tumour cell; anticancer drug; treatment; cancer; antiproliferative; anticoestrogen; progestogen; antiandrogen, testosterone inhibitor; anti-invasion agent; growth factor inhibitor; antimetabolite; antibiotic; alkjating agent; antimitotic agent; radiotherapy;
                                                                                                                                           Thymidylate synthase; antisense oligonucleotide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; Fig 7; 53pp; English.
                                                                                                           Human thymidylate synthase DNA.
             AAX24270 standard; DNA; 566
                                                                                                                                                                                                                        topoisomerase inhibitor; ss.
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                                                                           02-JUL-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                      (ISIS-) ISIS PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1999-254708/21
                                                                                                                                                                                                                                                            Homo sapiens
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AAX24270
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                                                          The present invention provides a novel method of estimating the susceptibility of an individual to a developmental disorder using genetic and environmental variables. The method can be used in the diagnosis, prevention and treatment of disorders such as schizophrenia, spina bifida cystica, Tourette's syndrome, bipolar illness, autism, conduct disorders, attention deficit disorder, obsessive compulsive disorder, chronic
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                                                                                                                                                                                                                                           Score 613.2; DB 22; Length 18596;
Pred. No. 2e-149;
0; Mismatches 63; Indels 6;
                                                                                                                                              attention deficit disorder, obsessive compulsive disorder, ch. multiple tic syndrome and learning disorders such as dyslexia
                                                                                                                                                                                             Sequence 18596 BP; 4521 A; 3991 C; 4479 G; 5605 T; 0 other;
                               Disclosure; Page 125-131; 156pp; English.
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nilarity 90.6%;
Conservative 0
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Matches 667;
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Vincent MD;

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98GB-0012140. 97GB-0020107. 97GB-0022012.

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This invention describes novel antisense oligonucleotides targeted to sequences in the 3' end of thymidylate synthase (TS) mRNA. Such oligonucleotides are cytostatic on their own when administered to human tumour cell lines, and also enhance the toxicity of anticancer drugs such as Tomudex administered to those cells. In addition, antisense oligonucleotides targeted to 5' sequences induce TS gene transcription. The antisense oligonucleotides are used in a method for the
                                                                                                                                                                                                                                                                                                              The antisense oligonucleotides are also used in the production of a medicant for the treatment of cancer, either separately or in conjunction with a therapeutic agent such as thymidylate synthase (TS) inhibitors
                                                                                                                                                                                                                                                                         treatment of cancer (or a method for providing antiproliferative effect)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  agents (e.g. antioestrogens, (anti)progestogens, antiandrogens, testosterone inhibitors, anti-invasion agents, growth factor inhibitors,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1031 tggaaatggctgtttagggtgctttcaaaggagctCgaaggatattgtcagtctttaggg 1090
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            antitumor antibiotics, alkylating agents, antimitotic agents,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 566 BP; 156 A; 101 C; 135 G; 174 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 topisomerase inhibitors, etc.), or radiotherapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               etc.); antiproliferative/antineoplastic agents
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                                                        19102 aattoatacaatgggggatgcacatatttacttgaatcatatagatgctttaaaagtgca 19161
                                                                                                                                                                                                                                                                                                                                                                    18862 taaaaccaaaacccagaaagccgacgaatgattatatcgtcttggaatccaaaggatatccc 18921
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Macaca mulatta rhadinovirus 1757; RRV; rhesus macaque rhadinovirus; Macaca mulatta rhadinovirus 1757; RRV; rhesileukin 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Macaca mulatta rhadinovirus 17577 (RRV) genome sequence SEQ ID NO:1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present invention describes a novel rhesus macaque rhadinovirus
                                      tetgatggcgctgcctccatgccatgccctctgccagttctatgtggtgaacagtgagct
                                                                                                                                                                                            cagetaegeeetgeteaegtaeatgattgegeaeateaegggeetgaageeaggtgaett
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                                                                                                                                                                                                                                                                                                                                                                                                                Method for checking absence of mutation at specific positions of varicella virus genome for quality control of attenuated live varicella
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                                                              Oka strain; pox vaccine; vaccine; poxvirus disease; chickenpox;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 125157;
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                          of the Varicella virus Oka strain
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Pred. No. 2.1e-95;
                                                                                                                                                                                                                                                                                                                                      Yamanishi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; Page 106-150; 158pp; Japanese.
                                                                                                                                                                                                                                                                                                                                      Takahashi M,
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66.5%;
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                            Nucleotide sequence
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                                                                                                    Zaricella virus
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Length 1014;
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                         Indels
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            4.8e-91;
Score 387.4; D
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0; Mismatches
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Kaposi's sarcoma; acquired immune deficiency syndrome; AIDS; DHFR; Bcl-2; dihydrofolate reductase; LUR; long unique region; vaccine; prophylaxis; diagnosis; treatment; HHV8; complement binding protein; vCBP; SSBP; ssDNA binding protein; transport protein; glycoprotein B; pol; vIL-6; DNA polymerase; vIral interleukin-6; BHV4-IEI I; thymidylate synthase; vMIP-II; BHV4-IEI II; vMIP-I; capsid protein I; tegument protein I; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            capsid protein I, ORF18 and ORF19 which encodes Tegument protein I. KSHV is a new human Herpesvirus (HHV8) believed to cause Kaposi's sarcoma (KS) which is the most common form of neoplasm occurring in persons with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This sequence is a fragment of the Kaposi's sarcoma-associated herpesvirus (KSHV) LUR (long unique region). This fragment contains coding regions for KI, ORP4 which encodes the complement binding protein v-CBP, ORF6 which encodes a sSDNA binding protein (SSBP), ORF7 which encodes a transport protein, ORF8 which encodes glycoprotein B, ORF9 which encodes DNA polymerase (pol), ORF0, ORF10, FMICh encodes winch encodes DNA polymerase (pol), ORF0, ORF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   which encodes VMIP-I, K7, ORF16 which encodes Bcl-2, ORF17 which encodes
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21023 GECGICINGGCITTGGCCCCCGAGGIIGACCCITGTICGATTCAGCATGAGGTAACTGGG 20964
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.larity 63.5%; Pred. No. 2.7e-90;
Conservative 0; Mismatches 341;
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                                                                                                                                                                                                                                                                                                                                                                                                                                          Kaposi's sarcoma-associated herpesvirus
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                                                                                                                                                                       XSHV LUR DNA (nucleotides 1-35,100)
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AAV73802 standard; DNA; 35100
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RESULT 10 AAV73802/c

the Kaposi's sarcoma-associated herpes virus (KSRY), KSHY is also known as human herpes virus 8 (HHV8). This sequence contains the DNAs of the invention which encode KSHY polypeptides selected from: (a) viral complement-binding protein; glycoproteins B, W or Li, (c) viral TRE 1; (d) complement-binding protein; glycoproteins B, W or Li, (d) capsid protein IV encoded by ORF65; and (e) immediate early protein encoded by ORF73. Labelled probes for the nucleic acid, proteins encoded by it, and antibodies (Ab) specific for the proteins are useful for detecting HHV8, specifically for diagnosis of Kaposi's sarcoma, in body of it, and antibodies (Ab) specific for the proteins are useful for detecting HHV8, specifically for diagnosis of Kaposi's sarcoma, in body of thicks or tissue samples. HHV8 infections can be treated with antisense or triplex forming moleonies or agents that bind specifically to the protein can be used in protective vaccines. Ab may also be used to differentiate between lymphomas, and HHV8 may be implicated in many other lymphoproliferative diseases such as lymphomas, lenkemia, the promession mycosis fungaides. Cells and animals containing the contein as targets for antiviral drugs, e.g. dihydrofolate reductase gene can be inhibited with methotrexate. These can also be used to determine to the immune status of a patient infected with HHV. HHVB derived protein cells and an also be used to determine the immune status of a patient infected with HHV. HHVB derived protein cells in the immune status of a patient infected with HHV. HHVB derived protein cells and a treated as containing the cells and an also be used to determine the immune status of a patient infected with HHV. HHVB derived protein cells in the immune status of a patient infected with HV. HHVB derived protein cells the immune status of a patient infected with HV. HVB derived protein cells in the immune status of a patient infected with HV. HVB derived as containing the cells anoted in the cells and an infection of the cells and an infection sequence represents the long unique region and terminal repeat of open reading frames

Sequence 137507 BP; 32579 A; 37795 C; 35758 G; 31375 T; 0 other;

ó; 20663 GCGCACAGAAGGGAGGGGGATTTGGGACTGTTTACGGTTTCCAGTGGAGGCACTTTGGG 20604 GCGGCGTACGTGGACGCGGATGCTGACTATACAGGCCAGGGGTTTGACCAATTGTCGTAC 20544 20543 ATTGTGGATTTAATAAAAAATAATCGCACGATAGAAGAATCATTATGTGTGCGTGGAAC 20484 20483 CCGGCGGACTIGICGTIGAIGCCGCTICCGCCCTGICACTIGITAIGICAATITIAIGIA 20424 21023 GOCGICTIGGCTTIGGCCCCCGAGGTIGACCCTIGTICGATICAGCATGAGGTAACTGGG 20964 20783 gracrecaagacrecrirgerricreaagggagracreacrecagggagcrirrcaaga 20724 115 geoggeteggagetgeeggeeggeettgeeeceeggeagaaggaggaeggagg 174 175 ccgcgtccgccgcacggggagctgcagtacctgggggcagatccaacatcctccgctgc 234 295 cgctacagcctgagagatgaattccctctgctgacaaccaaacgtgtgttctggaagggt 354 gttttggaggagttgctgtggtttatcaagggatccacaaatgctaaagagctgtcttcc 414 aagggagtgaaaatctgggatgccaatggatcccgagctttttggacagcctgggattc 474 Gaps 20963 GCTGAGACGCCCCACGAGGAACTTCAGTATCTCAGGCAGTTGAGGGAAATTTTGTGCCGT ggcgtcaggaaggacgacgcacggcaccggcaccctgtcggtattcggcatgcaggcg 20843 AGGIATAGICIGGGGACCACITICCCTIACIAACCACAAAGCGGGIGTITIGGCGAGGC tecaccagagaagaagaggacttgggcccagtttatggcttccagtggaggcattttggg gcagaatacagagatatggaatcagattattcaggacagggagttgaccaactgcaaaga gtgattgacaccatcaaaaccaacctgacgacagaagaatcatcatgtgcgcttggaat Score 387.4; DB 19; Length 137507; Pred. No. 5.2e-90; ; 0 Indels 0; Mismatches 341; 25.2%; illarity 63.5%; Conservative (Similarity Best Local Sim Matches 592; Query Match 355 415 475 595 655 535 20603 235 g Ωp g ద g ζ g δž g δŽ q δž ŏ g ã δŽ Qŏ

715 gtgaacagtgagctgtcctgccagctgtaccagagtcgggagacatgggcctcggtgtg 774

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is. The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell 20423 GCTGACGGTGAGCTTTCCTGTCAGCTGTATCAGAGGTCGGGAGACATGGGTTTGGGAGTT 20364 20363 CCTTTTAACATIGCCAGCIATICCCTCTTAACITAIAIGCTTGCTTGCTTGTTACTIGGTGTT 20304 capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of 20303 AGACCCGGGGGGTTTATTCACACGTTGGGAGATGCCCACATCTACAAACGCATATAGAG 20244 The invention relates to an isolated nucleic acid detection reagent insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA 955 aaagttgagaaaattgatgacttcaaagctgaagactttcagattgaagggtacaatccg cettteaacategecagetacgecetgeteacgtacatgattgegeacateacgggeetg ccactgaaaattcagcttcagcgagaacccagacctttcccaaagctcaggattcttcga 20243 CCACTACGGCTGCAGCTGACGCGCACTCCACGTCCCTTTCCGCGCCTGGAGATACTCCGG 835 aagccaggtgactttatacacactttgggagatgcacatatttacctgaatcacatcgag Drosophila melanogaster expressed polynucleotide SEQ ID NO 11762. developmental biology; cell signalling; insecticide; Claim 1; SEQ ID NO 11762; 21pp + Sequence Listing; English. (ABL01840-ABL16175) and the encoded proteins at ftp.wipo.int/pub/published_pct_sequences. 20123 CATCCTACCATTCGTATGGAAATGGCAGTATAG 20091 1015 catccaactattaaaatggaaatggctgtttag 1047 EW; Myers discloses genomic DNA sequences Li PWD, ABL05760 standard; cDNA; 2966 23-MAR-2001; 2001WO-US09231. 2000US-191637P. 2000US-0614150. (first entry) pharmaceutical; gene; ss Drosophila melanogaster. Venter JC, Adams M, (ABB57737-ABB72072). WPI; 2001-656860/75 (PEKE) PE CORP NY. P-PSDB; ABB61657 WO200171042-A2. 23-MAR-2000; 11-JUL-2000; interactions 27-SEP-2001. 26-MAR-2002 Drosophila; ABL05760; 12 895 775 ABL05760 g ద g οp g δŽ Qλ 엄 ă δŏ QY

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02-JUL-1999;
22-SEP-1999;
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Sequences AAA7722-A78199 represent 478 cDNAs encoding proteins or portions of proteins which are associated with human colon tumours. The invention also specifically discloses 8 human colon tumour proteins (AAB11897-B11904). The nucleic acids, the polypeptides they encode, and antigen presenting cells (APCs, preferably dendritic cells) expressing acting typeptides may be used in vaccines that target tumour cells, especially colon tumour cells. Thereby inhibiting the development of cancer. T-cells specific for the polypeptide expressed by the APC are used to remove tumour cells from biological samples, sepecific for the polypeptide can then be used to inhibit cancer development. CD4+ and/or fractions thereof. The sample or the isolated T-cells specific for the polypeptide can then be used to inhibit cancer development. CD4+ and/or colls from a patient may be incubated with a polypeptide, to cause the proliferation of specific T-cells. The T-cells can be consent the polypeptides may be used to determine the expression level cancer cells are present. Such diagnostic methods may also be used to monitor the progression of a cancer by separating the processes at time intervals, and comparing the current result to prevelous results. The intervals.
New colon tumor polypeptides used to inhibit the development of cancer, especially colon cancer, and for diagnosing and monitoring the progression of the cancer -
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Pred. No. 8.8e-79;
0; Mismatches 4; Indels 0;
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                                                                           Claim 1; Page 218; 229pp; English.
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98.8%;
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Human; immunotherapy; diagnosis; colon cancer; colon tumour;

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AL57329 AL57329
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BF690478 602186947
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Series: IRAL Plate: 4 Row: h Column: 10
                                                                AL571469 AL571469
AL575435 AL575435
AL172370 AU142370
AU117269 AU117269
BE597722 G03248376
BM475928 AGENCOURT
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Contact: nisc_mgc@nhgri.nih.gov
Shevchenko,Y., Wetherby,K.D., Beckstrom-Sternberg,S.M.,
Benjamin,B., Blakesley,R.W., Bouffard,G.G., Brinkley,C., Brooks,S.,
Dietrich,N.L., Guan,X., Gupta,J. Ho,S.-L., Karlins,E., Legaspl,R.,
Lim,M., Maduro,Q.L., Mastiello,C., Mastian,S.D., McCloskey,J.C.,
McDowell,J., Pearson,R., Snyder,B., Stantripop,S., Thomas,P.J.,
Tlongson,E.E., Touchman,J.W., Tsurgeon,C., Vogt,J.L., Walker,M.A.,
                  BG575942 602598373
                                                    BM467591 AGENCOURT
                                                                                                                                                                                                                                                                                                                BF968509 602271291
                                 BM472540 AGENCOURT
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1533)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Direct Submission Submitted (07-DEC-2001) National Institutes of Health, Mammallan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: ggapbs-rémail.nih.gov
Tissue Procurement: DCTD/DTP
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: National Institutes of Health Intramural
Sequencing Center (NISC),
Gaithersburg, Maryland;
                                                                                                                                                                                                                                                                                                                                                                                                                  linear
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Homo sapiens, clone IMAGE:3141419, mRNA.
BC018858
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BI59789
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BM459789
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AL551817 AL551811
                                                                               July 26, 2002, 07:45:16; Search time 3006.25 Seconds (without alignments) 6896.074 Million cell updates/sec
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             GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
                                                          OM nucleic - nucleic search, using sw model
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      /tissue_type="placenta"
/fissue_type="placenta"
/note="Vector: pcMvSPORT 6; Site_1: NotI; 1st strand cDNA
was primed with a NotI-oligo(dT) primer. Five prime end
enriched, double-stranded cDNA was digested with Not I and
cloned into the Not I and Eco RV sites of the pcMvSPORT 6
vector. Library was normalized. Library was constructed by
Life Technologies. Contact: Feng Liang Life Technologies,
a division of Invitrogen 9800 Medical Center Drive
Rockville, Maryland 20850, USA Fax: (1) 301 610 8371
Email : fliang@lifetech.com URL:
http://fulllength.invitrogen.com"

98 a 253 c 217 g 318 t 3 others
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Pred. No. 2.1e-225;
2; Mismatches 7;
/clone_lib="LTI_NFL006_PL2"
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99.0%;
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cloned into the Not I and Eco RV sites of the pCMYSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies. Contact: Fend Liang Lie Technologies, a division of Invitrogen 9800 Medical Center Drive Rockville, Maryland 20850, USA Fax : (1) 301 610 8371 Email : fliang@lifetech.com URL : http://fullength.invitrogen.com; 9 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /tissue_type="placenta" //tissue_type="placenta" //note="Yector: pChNYSPORF 6; Site_1: NotI; 1st strand cDNA was primed end was prime tha NotI-oligo(dT) primer. Five prime end enriched, double-stranded cDNA was digested with Not I and
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Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
Unpublished (2001)
                                                                                                                                                                                                                                                            1451
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                                                                                                                  185 AIGTGCATTICAATCCCACGTACTIATAAAGAAGGTIGGTGAATTICACAAGCTATTIT 126
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Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
                                                                        tgotgaggttatgaacaaagtgaggagaatgaaatgtatgtgotottagcaaaacatgt
                                                                                                                                                                  DB 9; Length 1077;
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/db_xref="taxon:9606"
/clone="cS0D1008YH21"
/clone_lib="LTI_NFL006_PL2"
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1. 1077
/organism="Homo sapiens"
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574
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                                                                                                                                                                                                                                                               GAGACATGGGCCTCGGTGTGCCTTTCAACATCGCCAGCTACGCCCTGCTCACGTACATGA 780
                                                                                                                                     601 TCATCATGTGCGCTTGGAATCCAAGAGATCTTCCTCTGATGGCGCTGCTCCATGCCATG
                                                                                                                                                                                           841 ITTACCTGAATCACATCGAGCCACTGAAAATTCAGCTTCAGCGAGAACCCAGACCTTTCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr. Location/Qualifiers
 515 tccagtggaggcattttggggcagaatacagagatatggaatcagattattcaggacagg
                                                                                                                  coctotgccagttctatgtggtgaacagtgagctgtcctgccagctgtaccagagatcgg
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                                                         ttgcgcacatcacgggcctgaagccaggtgactttatacacactttgggagatgcacata
                           481 TCCAGTGGAGGCATTTTGGGGCAGAATACAGAGATATGGAATCAGGATTATTCAGGACAGG
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Mammalia, Eutheria, Primates, Catarrhini, Hon
1 (bases I to 1021)
I.W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
Unpublished (2001)
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BP 191 91006 EVRY cedex - France
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/db_xref="taxon:9606"
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AL562750
AL562750.1 GI:12911478
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AL562750/C
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        624 CATCGAGCCACTGAAAATTCAGCTTCAGCGAGAACCCAGACCTTTCCCAAAGCTCAGGAT 565
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                                                                                                                 Length 1021;
                                                    others
                                                                                                                                                   Indels
Drive Rockville, Maryland 20850, USA 8371 Email: filang@lifetech.com URL http://fulllength.invitrogen.com" 230 c 203 g 307 t 5 ot
                                                                                                                 Score 945.2; DB 9;
Pred. No. 2.9e-202;
3; Mismatches 16;
                                                                                                                  61.5%;
nilarity 98.0%;
Conservative 3.
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1 (bases 1 to 938)
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/clone_lib="LTI_FL002_PL1"
/lab_inost="DH108"
/note="Organ: placenta: Vector: pCNVSPORT 6; lst strand
cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-stranded cDNA was digested with Not I
and cloned into the Not I and Eco RV sites of the
PCMVSPORT 6 vector. Library was constructed by Life
Technologies. Contact: Feng Liang Life Technologies, a
division of Invitrogen 9800 Medical Center Drive Rockville
'Maryland 20850, USA Fax: (1) 301 610 8371 Email:
filang@lifetech.com URL:
filang@lifet
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was primed with a Notrollgo(dT) primer. Five prime end enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the pCMNSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies. Context: Feng Liang Life Technologies. Context: Feng Liang Life Technologies. Rockville, Maryland 20850, USA Fax: (1) 301 610 8371 Email: fliang@lifetech.com URL: http://fullength.invitrogen.com "I others" of 289 c 259 g 188 t 1 others
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/db_xref='taxon:9606"
/clone='cSoD1060xE04"
/clone_lib="LTI_NFLOG_FL2"
/tissue_type='placenta"
/note="Vector: pCWV5PORT 6; Site_l: Not!; 1st strand cDNA
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938 bp mRNA linear EST 16-FE AL551990 LT_NFL006_PL2 Homo sapiens CDNA clone CSODIO60YEO4 prime, mRNA sequence.
AL551990
AL5511990.1 GI:12890459
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BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
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Mammalia; Eutheria; Primates;
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was primed with a Not1-coligo(dT) primer. Five prime end
enriched, double-stranded cDNA was digested with Not I and
cloned into the Not I and Eco RV sites of the pcMYSPORT 6
vector. Library was normalized. Library was constructed by
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a division of Invitrogen 9800 Medical Center Drive
Rockville, Maryland 20850, USA Fax : (1) 301 610 8371
Email : fillang@lifetech.com URL:
http://fullang@lifetech.com URL:
http://fullang@lifetech.com URL :
6 others
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Manmalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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Genoscope - Centre National de Sequencage
BP 191 91006 EWYX cedex - France
BP 191 seqrefégenoscope.cns.fr, Web : www.genoscope.cns.fr.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        Li, W.B., Gruber, C., Jessee, J. and Polayes, D. Full-length cDNA libraries and normalization
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 918; DB 9; I
Pred. No. 3.7e-196;
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/db_xref="taxon:9606"
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98.8%;
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AL550812
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COMMENT
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TITLE
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SOURCE
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Catarrhini; Hominidae; Homo.
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Mammalia; Eutheria; Primates; Catarrhini; Hon
1 (Dases I to 932)
Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
Unpublished (2001)
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AL526821 LTI_NFL003_NBC3
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AUTHORS NIH-MGC http://mgc.nci.nih.gov/. TITLE National Institutes of Health, Mammalian Gene Collection (MGC) JOGRNAL Contact: Robert Strausberg, Ph.D. Email: cgapbs-rémail.nih.gov Tissue Procurement: Lou Staudt CONA Library Preparation: Life Technologies, Inc. CONA Library Preparation: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LiML at: http://image.lihl.gov g column: 17 High quality sequence stop: 687. High quality sequence stop: 687. High quality sequence stop: 687. FEATURES 1. 1045 //clone="Image: Lympona" cell line" //lab_host="Image: Lympona" cell line" //lab_host="Image: Lympona" cell line" //lab_host="Image: Lympona" cell line" //lab_host="Uniph" //pector: pCMV-SPORT6; Site_I: Not!;	Site_2: SalI; Cloned unidirectionally; Oligo-dT primed. Average insert size 1.867 kb. Library enriched for full-length clones and constructed by Life Technologies. Note: this is a NIH_MGC Library." BASE COUNT 242 a 297 c 286 g 220 t ORIGIN Query Match 58.0%; Score 890.2; DB 10; Length 1045; Best Local Similarity 96.6%; Pred. No. 7e-190; Matches 986; Conservative 0; Mismatches 23; Indels 12; Gaps 7;	ccgccgccacttggctgcctccgtccgcgcgcacttggctgcctccgtccc 92	131 gatccaacatcctccgctgcggcgtcaggacggacggcagggagacggaccggaccgt	OY 393 aaatgotaaagagtettccaaggagtgaaatctgggatgccaaggatcccgaga 452
	Oy 486 agaagggaacttgggcccagtttatggcttccagtggaaggcattttggggcagaatacag 545	541 CATCAAAACCAACCCTGACGACAGAAGAATCATCATGTGGGGCTTGGAATCCAAGAGATCTGGGGCTTGGGAATCCAAGAGATCTGGGGGCGCTCCAAGAGAATCTGGGGGGGCGCTGCCAGGGGGGGG	721 GCCAGCTACGCCTGCTCACAGGATGCAGGATCAGGAGCCAGGGCCTGGAGCCAGGAGCAGGAGCAGGAGCAGGAGCAGGAGCAGGAGCAGGAGCAGGAGCAGGAGCAGGAGCAGGAGCAGGAGCAGGAGCAGGAGCAGGAGCAGGAGCAGGAGCAGGAGCAGGAGAGCAGGAGCAGGAGAGCAGC	RESULT 13 BM478045 LOCUS DEFINITION AGENCOUTE_6482920 NIH_MGC_85 Homo sapiens cDNA clone IMAGE:5552680 S, mRNA sequence. BM478045.1 GI:18527087 BM478045.1 GI:18527087

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Search completed: July 26, 2002, 15:13:16 Job time: 26880 sec
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was primed with a Not1-oligo(dT) primer. Five prime end
enriched, double-stranded cDNA was digested with Not I and
cloned into the Not I and Eco RV sites of the pcMYSPORT 6
cloned into the Not I and Eco RV sites of the pcMYSPORT 6
Life Technologies. Contact: Feng Liang Life Technologies,
a division of Invitrogen 9800 Medical Center Drive
Rockville, Maryland 20850, USA Fax : (1) 301 610 8371
Emmil: filang@lifetech.com URL:
http://tullang@lifetech.com URL:
http://tullang@lifetech.com URL 3 others
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                             AL578646 AL7_NFLO06_PL2 Homo sapiens CDNA clone CSODK004YL08 3
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1 (bases 1 to 906)
11, W.B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished (2001)
Contact: Genoscope
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BP 191 91006 EVRI cedex - France
Email: segrefégenoscope.cns.fr. Web : www.genoscope.cns.fr.
Location/Qualifiers
1. 906
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/db_xrefe"taxon:9006"
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                                                                                          AL578646.1 GI:12942922
                                                           prime, mRNA sequence.
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RESULT 15
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KEYWORDS
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Title: Perfect score:

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AX281791 Sequence
BC013919 Homo sapi
AX069365 Sequence
AX060139 Mus muscu
M13019 Mouse thymi
L12138 Rattus norv
M30774 Mouse thymi
AX144965 Sequence
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AX34101 Sequence
AX34101 Sequence
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U20824 Equine herp
AF087411 Rhesus ma
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U75698 Kaposi's sa
AF307518 Human her
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AR0783411

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369 c 399 g
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                                                                                 (aa 1-313)"
                                                                                                                                                                                                                                                                                               ; Pred. No. 4.3e-307; 0) Mismatches 3: T-3
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Arche="pot. polyadenylation signal"
1519. .1524
/note="pot. polyadenylation signal"
  /note="pot. stem-loop structure"
70. .72
/note="direct repeat 1"
                                                                                                                                                                                                                                                  /note="polyadenylation site"
369 c 399 g 378 t
                                                                        106. .1047
/note="thymidylate synthase
                                                                                                                         /db_xref="SWISS-PROT:P04818"
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                                          104. .106
/note="direct repeat 1"
106. .1047
                                                                                             /codon_start=
                                                                                                                                                                                                                                                                                                     99.7%;
99.8%;
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Matches 1533; Conservative
                                 .103
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               repeat_region
                                                      repeat_region
                                                                                                                                                                                                                     misc_feature
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1402 tagaatattttaagaatttcacaagetattccctcaaatctgagggagctgagtaacacc 1461 gacatcacgggctgaagccaggtgactttatacacactttg atttttaaggatgttgccactggcaaatgtaactgtgccagt gtgttctggaagggtgtttggaagagttgctgtggtttatc tggaggcattttggggcagaatacagagatatggaatcagat ctcaggattcttcgaaaagttgagaaaattgatgacttcaaa aagaaggttggtgaatttcacaagctatttttggaatatttt gacagcctgggattctccaccagagaagaaggggacttgggc atgtgcgcttggaatccaagagatcttcctctgatggcgctg tgccagttctatgtggtgaacagtgagctgtcctgccagctg

28 1 1 1 8 8 8 1 1 8 8 8 1 8 1 8 1 8 1 8	Qy 586 otgoaagagtgattgacaccatoaaaaccaacctgacgacagaaatcatgtgc 645	Oy 886 cacategagccactgaaattcagcttcagcgagaacccagaccttcccaagctcagg 945	RESULT 7 AB077208 LOCUS LOCUS LOCUS DEFINITION AB077208 AB077208 ACCESSION AB077208 TETVELON RETWORDS SOURCE Homo sapiens cell_line:KATO III. ACCESSION AB077208 TETVENCE CORGANISM Homo sapiens cell_line:KATO III cDNA to mRNA. ORGANISM Homo sapiens CORGANISM HOMO SAPIENS TITLE CORGANISM TITLE CORGANISM C
110 taaaagttcttttgctctaaaagaaGaaggaactaggtcaaaaatctgtcc 1110 taaaagttctttttgctctaaaagaaGaaggaactaggtcaaaaatctgtcc 1110 taaaagttctttttgctctaaaagaaGaaggaactaggtcaaaatctgtcc 110 taaaagttctttttaaggatgttgcacacaggcaaatgtaactggccagf 110 tcagttattaatttttaaggatgttgcacacaggcaaatgtaactggccagf 111	OY 1410 transpartrocased cost cost casa to the state of t	ata; Vertebrata; Butel. rhini; Hominidae; Homo ted enzymes	DASE COUNT 236 a 247 c 257 g 202 t construction of 242; DB 6; Length 942; DB 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0; DB 1470CTG1G2G1G1G1[

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/product="ths mRNA"
38. .961</pre>
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FNIASTALLTYMTAHITGLQPGPFVHTLGDAHIYLNHIEPLKIQLQREPRPFPKLKIL
RKUTIDDEKVEDPGTVPHPTIKMEMAV"
RVGIIDDFVEDPGTVPHPTIKMEMAV"
226 c 253 g 237 t
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WDANGSRDFILDSLGFSARQEGDLGFVYGFQWRHFGAEYKDMDSDYSGQGVDQLQKVID
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                                                                                                                                                                                                                    /translation="MLVVGSELQSDAQQLSAEAPQHGELQYLRQVEHILRCGFKKEDR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          246 ggacgaccgcaccggcaccctgtcggtattcggcatgcaggcgcgctacagcct 305
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                                                                                                                                                                                                                                                                                                                                                                                     Score 711.4; DB 10; Length 986; Pred. No. 3.5e-137;
                                                                                                                                                                    /product="Unknown (protein for MGC:28246)"
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                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches 131;
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50. .973
                                                                                                                                                      /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                      46.3%;
85.8%;
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/processister.e.a.
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FULASYALLTYMIAHITGLQPGDFVHTLGDAHIYLNHIEPLKIQLQRESPPFFFKILL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ROD 27-APR-1993
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1 (bases 1 to 961)
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MOUSE thymidylate synthase pseudogene mRNA, complete cds.
M30774
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Li, D. and Johnson, L.F.
A mouse thymidylate synthase pseudogene derived from an aberrantly processed RNA molecule Gene 82, 363-370 (1989)
                                                                                                             gagaaaattgatgacttcaaagctgaagactttcagattgaagggtacaatccgcatcca 1020
                                                             481 agagaagaaggggctttgggcccagtttatggcttccagtggaggcattttggggcagaa 540
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Universal to 18596)
Johnson, W.G. and Stenroos, E. Scott.
Johnson, W.G. and Stenroos, E. Scott.
Methods for diagnosing, preventing, and treating developmental
disorders due to a combination of genetic and environmental factors
Patent: US 6210950-A 11 03-APR-2001;
Location/Qualifiers
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tacagagatatggaatcagattattcaggacagggagttgaccaactgcaaagagtgatt
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AR144965
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Pred. No. 9.8e-117
        Patent: WO 0194629-A 1191 13-DEC-2001;
Avalon Pharmaceuticals (US)
Location/Qualifiers
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/organism="Homo sapiens"
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AX330906

DEFINITION

LOCUS

ACCESSION

Sequence 1415 from Patent W00194629. AX330906

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Young, P.E., Augustus, M., Carter, K.C., Ebner, R., Endress, G., Horrigan, S., Soppet, D.R. and Weaver, Z. Cancer gene determination and therapeutic screening using signature
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              Enkaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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/db_xref="taxon:9606"
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Listing first 45 summaries
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Copyright (c) 1993
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                                                                                                  PREVENTING, AND TREATING
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                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                         Score 1163.8; DB 4;
Pred. No. 4.3e-194;
0; Mismatches 10;
                                                             APPLICANT: Johnson, William G.
APPLICANT: Stenroos, Edward S.
TITLE OF INVENTION: METHODS FOR DIAGNOSING, PRI-
TITLE OF INVENTION: DEVELOPMENTAL DISORDERS
FILE REFERENCE: 601-1-057
CURRENT APPLICATION NUMBER: US/09/318,448
CURRENT FILING DATE: 1999-05-25
NUMBER OF SEQ ID NOS: 46
US-09-318-448-11
; Sequence 11, Application US/09318448
; Patent No. 6210950
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                       98.0%;
99.1%;
                                                                                                                                                                                                     SOFTWARE: PatentIn Ver. 2.0 SEQ ID NO 11
                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                          TYPE: DNA ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                        18596
                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Sim
Matches 1176;
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Sequence 358, App Sequence 3, Appli

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US-09-385-982-358 US-09-797-906-3 US-08-646-301A-1 US-08-481-968A-4

84495 11288 11288

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PatentIn Ver. 2.0
      ENERAL INFORMATION...
APPLICANT: Ford, John
APPLICANT: Mulero, Julio
Yeung, George
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                                                                                                                                                                                                 PRIOR APPLICATION NUMBER:
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           GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 16.2%; Score 191.8; DB 4; Length 14747; Best Local Similarity 77.1%; Pred. No. 1.8e-25; Matches 266; Conservative 0; Mismatches 59; Indels 20; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; OTHER INFORMATION; n = adenosine or guanine or cytosine or thymidine US-09-608-285A-42
                                     TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO CD39-LIKE TITLE OF INVENTION: POLYPEPTIDES FILE REFERENCE: 28110/36570
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                                                                                             CURRENT APPLICATION NUMBER: US/09/608,285A
CURRENT FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: 09/583,231
PRIOR PILING DATE: 2000-06-26
PRIOR PELICATION NUMBER: 09/557,800
PRIOR PLILNG DATE: 2000-04-25
PRIOR PLILNG DATE: 2000-04-25
PRIOR PLILNG DATE: 2000-04-15
PRIOR PLILNG DATE: 1090-08-09
PRIOR PLILNG DATE: 1099-08-09
PRIOR APPLICATION NUMBER: 09/370,265
PRIOR PLILNG DATE: 1999-07-06
PRIOR APPLICATION NUMBER: 09/370,447
PRIOR PLILNG DATE: 1999-07-09
PRIOR PLILNG DATE: 1999-07-04
PRIOR PLILNG DATE: 1999-07-04
PRIOR PLILNG DATE: 1998-07-04
PRIOR PLILNG DATE: 1998-07-24
PRIOR PLILNG DATE: 1998-07-24
PRIOR PLILNG DATE: 1998-07-24
PRIOR PLILNG DATE: 1998-07-24
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APPLICANT: Mulero, Julio APPLICANT: Yeung, George
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LENGTH: 14747
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TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO CD39-LIKE ITTLE OF INVENTION: POLYPEPTIDES FILE REFERENCE: 28110/36570
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                                                                                           CURRENT APPLICATION NUMBER: US/09/608,285A CURRENT FILING DATE: 2000-06-30
                                                                                                                                                                                                                                                                                                                                                                                                                           PCI/US99/16180
                                                                                                                                                                             PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 09/557,800
PRIOR PILING DATE: 2000-04-25
PRIOR FILING DATE: 2000-04-25
PRIOR PELING DATE: 2000-01-11
PRIOR PELING DATE: 2000-01-11
PRIOR FILING DATE: 1999-08-09
PRIOR FILING DATE: 1999-07-16
PRIOR APPLICATION NUMBER: 09/370,265
PRIOR APPLICATION NUMBER: 09/350,836
PRIOR FILING DATE: 1999-07-16
PRIOR PILING DATE: 1999-07-16
PRIOR PILING DATE: 1999-07-09
PRIOR APPLICATION NUMBER: 09/273,447
PRIOR APPLICATION NUMBER: 09/273,447
PRIOR FILING DATE: 1999-02-04
PRIOR FILING DATE: 1999-02-04
PRIOR FILING DATE: 1999-02-04
PRIOR FILING DATE: 1999-02-04
PRIOR FILING DATE: 1999-07-24
PRIOR FILING DATE: 1999-07-24
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NAME/KET: misc_feature
LOCATION: (14871)
OTHER INFORMATION: n = a or c or g or t
                                                                                                                                                               09/583,231
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16.2%; Score 191.8; DB 4; Length 15977; 77.1%; Pred. No. 1.8e-25;

Query Match Best Local Similarity

; Sequence 59, Application US/09608285A ; Patent No. 6335013

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947 atctcaggtgatccacccgcctcggcctcccaaagtgctgggattacaggtgtgagccac 1006
      888 tigiatititiagtagogac-agggictoaccaigitiggccaagoiggictigaaticoig 946
                                               331 aceteaggtgatecaccegecteggecececaaagtactaggattacaggegtgagecae 390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                E: KOHN & ASSOCIATES 30500 No. 6025183thwestern Highway, Suite 410
                                                                                                                                                                                                                                                                                                                               APPLICANT: Soreq, Hermona
APPLICANT: Zakut, Haim
APPLICANT: Zakut, Haim
APPLICANT: Shani, Moshe
IITLE OF INVENTION: TRANSGENIC ANIMAL ASSAY SYSTEM FOR
TITLE OF INVENTION: AMI'-CHOLINESTERASE SUBSTNACES
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LOCATION: 4089..22464
OTHER INFORMATION: /function= "ACHE Promotor"
OTHER INFORMATION: /standard_name= "ACHE Promotor"
                                                                                                                                                                      1007 catgoccagoctaccetttactactaatcaaagaaataa 1045
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/814,095
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          promotor, ACHE gene and ARS gene"
                                                                                                                               391 egegtecagegecetggeggtttttaateaagtagaaa 429
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: 2391.00066 TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "Cosmid inc
                                                                                                                                                                                                                                                                           Sequence 7, Application US/08814095
Patent No. 6025183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /number= 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: Montgomery, Ilene N.
REGISTRATION NUMBER: 38,972
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEPHONE: (248) 539-5050
TELEFAX: (248) 539-5055
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   35060 base pairs
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CHROMOSOME/SEGMENT: 7q22
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LOCATION: 22465..22537
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EDNESS: double
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                                                                                                                                                                                                                                                      US-08-814-095-7
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APPLICANT: Kent D. Taylor (Inventor)
APPLICANT: Maren T Scheuner (Inventor)
APPLICANT: Jarone I. Rotter (Inventor)
APPLICANT: Hillying Yang (Inventor)
TITLE OF INVENTION: Genetic Test to Determine
TITLE OF INVENTION: Genetic Test to Determine
FILE REFERENCE: PO 7 41878
CURRENT APPLICATION NUMBER: US/09/347,114A
                                                                                                                                        105 ggcggtctttttttttttttttttttttttttgggacagtcttgctcgcccag 164
                                                                                                                                                                                                                                                   61 gotggagtgcagtggcatgatctcggctcactgcaaggtccgcccgggctcatgcca 120
                                                                                                                                                                                                                                                                                                                                                121 ttetectgeeteageeteegagtagetgagattataggeaeetaeeaceaegeeegget 180
                                                                                                                                                                                                                                                                                                                                                                                       266 aattttgtanttttagtagagacgggggtttcaccatgttgtccaggctggtctngaac 325
                                                                                                                                                                                                                                                                                                                                                                                                                 326 tectgaceteaggtgatecaccegeeteggeeececaaagtaetaggattacaggegtga 385
                                                                                                                                                                                                                                                                                                            ttottotgoctcagoctcccaagtag-------ccaccacgcccagct 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             165 gctggagtacaatggtcggatcttggctcactgcaacctctgcctcccaggttcaagcaa 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      110 tettitittttttttttttttttttttgggacagtettgetetgtegeceaggetgg 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        230 ctgcctcagcctcccaagtag------230 ctgcctcagccagctaattt 270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          271 ttgtanttttagtagagacggggtttcaccatgttgtccaggctggtctngaactcctg 330
                                                                                                   42; Indels 20; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             57; Indels 20; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15.9%; Score 189; DB 4; Length 3867; 77.3%; Pred. No. 5.1e-25; Live 0; Mismatches 57; Indels 20
                                                     15.9%; Score 189; DB 4; Length 631; 80.3%; Pred. No. 4.6e-25; tive 0; Mismatches 42; Indels :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; Sequence 81, Application US/09347114A; Patent No. 6297014
                                                                                                 Matches 253; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         386 gccaccgcgtccage 400
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                                                                               Best Local Similarity
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US-09-385-982-354
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US-09-347-114A-81
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                                                          Query Match
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1238 TITIAGIAGAGACAGGGTTTCACCATGTTGGCCAGGCTGGTCTCGAACTCCTGACTCT 1179
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                                                                                                                                                                           277 ttttagtagaagggggtttcaccatgttgtccaggctggtctngaactcctgacctca 336
                                                      ---gecaccacgeccagetaa--tttttgtan 276
                                                                                                                                                                                                                                                                                                         337 ggtgatccacccgcctcggccccccaaagtactaggattacaggcgtgagccaccgcgtc 396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1418 TITATITATITATITITITAGATGGAGTCTCGCTCTGTCACCCAGGCTGGAGTGCAAT 1359
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15.9%; Score 188.8; DB 4; Length 2713;
81.9%; Pred. No. 5.4e-25;
Live 0; Mismatches 34; Indels 21; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              118 ttttttttttttttttttttgggacagtcttgctctgtcgcccaggctggagtacaat 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/09/154,602
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: RAB PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/916,901
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 6, Application US/09154602
Patent No. 6300472
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Hillman, Jennifer L. APPLICANT: Lal, Preeti APPLICANT: COrley, Neil C. APPLICANT: Shah, Purvi
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET: 3174 Porter Dr. CITY: Palo Alto
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STRANDEDNESS: single
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MEDIUM TYPE: Diskett
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CORRESPONDENCE ADDRESS:
                                               238 gcctcccaagta--
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US-09-154-602-6
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                                     8682 AGGIGAITCCACCCACCTCGGCCTCTCAAAGTACTGGGATTACAGGCATGAGCACCACCACA 8741
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8622 TITITAGIAGAGACAGGITITGCCATGITGGCCAGGCTGGTCTTGAACTCCTAACCTC 8681
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          -----gccaccacgcccagctaa-tttttgta 275
                                                                                                                              276 nttttagtagagaggggtttcaccatgttgtccaggctggtctngaactcctgacctc 335
                                                                                                                                                                                                                                                         336 aggtgatccacccgcctcggcccccaaagtactaggattacaggcgtgagccaccgcgt 395
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SULTWARE: DOS
SULTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/916,901
FILING DATE: Filed Herewith
PRIOR APPLICATION DATA:
FILING DATE:
FILING DATE:
ATTORNEY:
AT
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APPLICANT: Lal, Preeti
APPLICANT: Corley, Neil C.
APPLICANT: Shah, Purvi
TITLE OF INVENTION: RAB PROFEINS
NUMBER OF SEGUENCES: 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 6, Application US/08916901; Patent No. 5892012
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TELEPHONE: 415-855-055
TELEFAX: 415-845-4166
236 cagceteceaagta-----
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TYPE: nucleic acid
STRANDEDNESS: single
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REGISTRATION NUMBER: 3'
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Best Local Similarity
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US-08-916-901-6/c
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NAME/KEY: CDS
LOCATION: (4361)...(4507)
NAME/KEY: CDS
LOCATION: (4612)...(4737)
NAME/KEY: CDS
                                                                                                                                                                                                                                                          Best Local Similarity 73.1
Matches 275; Conservative
                                                                                                 TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
                                                                               LENGTH: 72604
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQ ID NO 45
LENGTH: 8447
                                                                                                                                                                                             US-09-268-992-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA
                                                                                                                                                                                                                                             Query Match
                                                                                                                                  FEATURE:
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APPLICANT: Chen, H.
APPLICANT: Freiner, N.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING
TITLE OF INVENTION: AND TREATING CHROMOSOME-18p RELATED DISORDERS
FILE REFERENCE: 7853-138
                                                                                                                                                                                                                                                                                                                                                                                                                      15.8%; Score 187.6; DB 1; Length 17327; 78.9%; Pred. No. 9.7e-25; Live 0; Mismatches 46; Indels 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/09/268,992
CURRENT FILING DATE: 1999-03-16
FEARLIER APPLICATION NUMBER: 09/236,134
EARLIER FILING DATE: 1999-01-22
FEARLIER APPLICATION NUMBER: 60/106,056
FEARLIER APPLICATION NUMBER: 60/108,312
FEARLIER APPLICATION NUMBER: 67/088,312
FEARLIER PILING DATE: 1998-06-05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 7, Application US/09268992
Patent No. 6342351
TELEPAX: (202)833-8716
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
                                               17327 base pairs
                                                                                                                                                                                                                                                                                                                                           exon
16397..17327
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Best Local Similarity 78.9
Matches 243; Conservative
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9745..16396
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754..9596
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621..753
                                                              NUCLEIC ACID
                                                                             STRANDEDNESS: bot
TOPOLOGY: linear
MOLECULE TYPE: DNA
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LOCATION:
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LOCATION:
FEATURE:
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LOCATION:
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LOCATION:
                                                                                                                                                                                                                                                                                                                                          NAME/KEY:
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US-07-906-871-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 13
US-09-268-992-7
                                                   LENGTH:
                                                                TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                37 gagactetgteteaaaaaaaaaaaaaaaaaaaagaeegeeagggeteaaacaaaaaaeetegga
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 72604;
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APPLICANT: Raftogianis, Rebecca B.
APPLICANT: Wood, Thomas C.
APPLICANT: Wood, Thomas C.
APPLICANT: Wood, Thomas C.
TITLE OF LINVENTION: SULFOTRANSFERASE SEQUENCE VARIANTS
FILE REFERENCE: 07039/118001
CURRENT APPLICATION NUMBER: US/09/167,681A
CURRENT FILLO BATE: 1998-10-07
NUMBER OF SEQ ID NOS: 52
SOFTWARE: FastSEQ for Windows Version 3:0
                                                                                                                                                                                                                                                                                                                                                      DB 4;
                                                                                                                                                                                                                                                                                                                                                    Score 187.2; DB 4
Pred. No. 1.2e-24;
0; Mismatches 80
EARLIER APPLICATION NUMBER: 60/078,044
EARLIER FILING DATE: 1998-03-16
NUMBER OF SEQ ID NOS: 84
SOFTWARE: FRASEEQ for Windows Version 3.0
SEQ ID NO 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                tcaagcaattcttctgcctcagcctcccaagtag
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                                                                                                                                                                                                            NAME/KEY: modified base
LOCATION: all n positions
OTHER INFORMATION: n=a, c, g, or t
                                                                                                                                                                                                                                                                                                                                                    15.8%; 73.1%;
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Search completed: \mathrm{July}\ 26, 2002, 17:48:22 Job time: 12551 sec
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                                                                                                                                                                                                                                                     110 tettttttttttttttttttttttttttgggacagtettgetetgtegeccaggetgg 169
                                                                                                                                                                                                                       52; Indels 20; Gaps
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                                                                                                                                                                                      Score 186; DB 4; Length 8453;
Pred. No. 1.8e-24;
0; Mismatches 52; Indels 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: 17q-Linked Breast and Ovarian Cancer TITLE OF INVENTION: Susceptibility Gene WINDBER OF SECURNCES: 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3: Venable, Baetjer, Howard & Civiletti, LLP 1201 New York Avenue, N.W., Suite 1000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/480,784
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Skolnick, Mark H.
Goldgar, David E.
Miki, Yoshio
Swenson, Jeff
Kamb, Alexander
Harshman, Keith D.
Shattuck-Eidens, Donna M.
Tavtigian, Sean V.
Wiseman, Roger W.
Futreal, P. Andrew
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1989 cacgctcagcctctttcttgttctatat 2016
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                                                                                                                                                                                      Query Match 15.7%;
Best Local Similarity 78.0%;
Matches 256; Conservative
                                         NAME/KEY: CDS
LOCATION: (6543)...(6638)
NAME/KEY: CDS
LOCATION: (7137)...(7316)
NAME/KEY: CDS
                                                                                                                   ; LOCATION: (7439)...(7553)
US-09-167-681-45
(4827)...(4925)
                CDS ...(6447)
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ADDRESSEE: Venable,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
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APPLICANT:
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APPLICANT:
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COUNTRY:
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                NAME/KEY:
                               COCATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 185.8; DB 1;
Pred. No. 1.9e-24;
0; Mismatches 49;
                                                                                                                                                                                                                                                                                                                                                  24884-109347
                                                                                                               PRIOR APPLICATION NOMER:
PRIOR APPLICATION NUMBER: US 08/308,104
FILING DATE: 16-SEP-1994
PRIOR APPLICATION NUMBER: US 08/300,266
FILING DATE: 0-SEP-1994
PRIOR APPLICATION NUMBER: US 08/300,266
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/289,221
FILING DATE: 12-AUG-1994
ATTORNEY/AGENT INFORMATION:
                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/409,305
FILING DATE: 24-MAR-1995
                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/348,824
FILING DATE: 29-NOV-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5725 TIGAGCCACCGTGCCCAGCAACC 5747
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                                                                                                                                                                                                                                                                                                                 NAME: Ihnen, Jeffrey L. REGISTRATION NUMBER: 28,957
                                                                                                                                                                                                                                                                                                                                                                  TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-962-4810
                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: 202-962-8300
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DNA (genomic)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGIH: 6769 base pairs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches 254; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: nucleic acid
STRANDEDNESS: double
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               linear
FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ANTI-SENSE: NO
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ADDRESSEE: Sterne, Kessler, Goldstein & Fox
STREET: 1225 Connecticut Avenue, N.W., Suite 300
CITY: Washington
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/906,871
FILING_DATE: 19920103
                                                                                                                                                                                                                                                                                                                                                                                                                                                      30169 GIGCCIGGCCCAGAGAGAIATTAATGAAAAAAAAA 30206
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REFERENCE/DOCKET NUMBER: 0627.2830004
IELECOMMUNICATION INFORMATION:
TELEPHONE: (202)833-7533
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US89/03051
PILING DATE: 13-JUL-1989
PRIOR APPLICATION DATA:
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APPLICATION NUMBER: US/07/816,289
FILING DATE: 03 JAN 1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/635,544
FILING DATE: 18-JAN-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US/07/224,035
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 15, Application US/07906871; Patent No. 5340739; GENERAL INFORMATION: APPLICANT: Avraham, Shalom APPLICANT: Avraham, Shalom
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 THEREOF
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FILING DATE: 13-JUL-1988
ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                tgcctcagcctcccaagta--
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ADDRESSEE: Sterne, K
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
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CLASSIFICATION:
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                                                                 -----gccaccacgcccagctaa--tttttgtan 276
                                                                                                                       277 ttttagtagagaggggtttcaccatgttgtccaggctggtctngaactcctgacctca 336
                                                                                                                                                                                               337 ggtgatccaccgcctcggccccccaaagtactaggattacaggcgtgagccaccgcgtc 396
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Mulligan, John T.
APPLICANT: Schellenberg, Gerald D.
TITLE OF INVENTION: GENE AND GENE PRODUCTS RELATED TO TITLE OF INVENTION: WERNER'S SYNDROME
NUMBER OF SEQUENCES: 209
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pred. No. 6.6e-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: No. 6090620tenburg Ph.D., Carol
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: 24,052.419
TELECOMMUNICATION INFORMATION:
TELEPRAN: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 79:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/08/781,891
FILING DATE: 27-DEC-1996
CLASSIFICATION: 800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 79, Application US/08781891
Patent No. 6090620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REGISTRATION NUMBER: 39,317
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nucleic acid
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Yu, Chang-En
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      single
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Washington
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                                                    238 gcctcccaagta-
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APPLICANT: Fu, Yi
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US-08-781-891-79
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APPLICANT:
APPLICANT:
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US-08-781-891-79
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LOCATION: 24090..25177
IDENTIFICATION METHOD: experimental
OTHER INFORMATION: /function= "(translation start:
OTHER INFORMATION: 24110)"
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OTHER INFORMATION: /function= "arsenite resistance
                                                                                                                                                                    NAME/KEY: exon
LOCATION: 25524..26009
LOCATION: 25524..26009
LOCATION: Periods experimental
OTHER INFORMATION: /gene= "ACHE"
OTHER INFORMATION: /gene= "ACHE"
                                                                                                                                                                                                                                                                                                                           NAME/KEY: exon
LOCATION: 27005..27274
IDENTIFICATION METHOD: experimental
OTHER INFORMATION: /evidence= EXPERIMENTAL
OTHER INFORMATION: /gene= "ACHE"
OTHER INFORMATION: /number= 4
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IDENTIFICATION METHOD: experimental
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OTHER INFORMATION: /gene= "ACHE"
OTHER INFORMATION: /number= 6
                                                                 OTHER INFORMATION: 24110)"

OTHER INFORMATION: /evidence= EXPERIMENTAL
OTHER INFORMATION: /gene= "ACHE"
OTHER INFORMATION: /Dumber= 2
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OTHER INFORMATION: /gene= "ACHE"
OTHER INFORMATION: /number= 5
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OTHER INFORMATION: /gene= "AR"
OTHER INFORMATION: /number= 3
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OTHER INFORMATION: /gene= "AR"
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OTHER INFORMATION: /gene= "AR"
OTHER INFORMATION: /number= 4
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OTHER INFORMATION: /number= 2
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OTHER INFORMATION: /gene= "AR"
OTHER INFORMATION: /number= 6
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LOCATION: 27255..28007
IDENTIFICATION METHOD:
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27385..27387
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28129..28131
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INFORMATION:
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                 LOCATION: complement (32569..32628)
OTHER INFORMATION: /gene= "AR"
OTHER INFORMATION: /number= 7
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OTHER INFORMATION: /gene= "AR"
OTHER INFORMATION: /number= 9
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OTHER INFORMATION: /gene= "AR"
OTHER INFORMATION: /number= 12
                                                                                                                                        LOCATION: complement (32386..32468)
OTHER INFORMATION: /gene= "AR"
OTHER INFORMATION: /number= 8
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OTHER INFORMATION: /gene= "AR"
OTHER INFORMATION: /number= 10
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CTHER INFORMATION: /number= 16
US-08-814-095-7
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OTHER INFORMATION: /number= 15
NAME/KEY: exon
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NAME/KEY: exon
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LOCATION:
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                                                                                  Db 11219 tettetteteeeetaeeetttttttttgagaeagagtettgetetgteaeeeaggetgg 11278
                                                                                                                                                                                                                                                                                                                   11458 acctcaggtgatccacccgcctcagcctcccaaagtgctaggattacaggcgtgagccac 11517
                                                                                                                           agtacaatggtcggatcttggctcactgcaacctctgcctcccaggttcaagcaattctt 229
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                                      tettittittittittittittittittitgggacagtettgetetgtogeecaggetgg 169
20; Gaps
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  59; Indels
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Disease and its Use
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  391 cgcgtccagcgccctggcggtttttaatcaagtagaaagctgca 435
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APPLICANT: Salbaum, Johannes; Masters, Colin;
APPLICANT: Beyreuther, Konrad
TITLE OF INVENTION: Promoter of the Gene for the
TITLE OF INVENTION: Human Precusor of the Alzhein
TITLE OF INVENTION: Disease and its Use
  0; Mismatches
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MEDIUM TYPE: Diskette, 3.50 inch, 1.44MB
MEDIUM TYPE: storage
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/325,745
FILING DATE: 19-0CT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/153,546
FILING DATE: 16-NOV-1993
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 14-AUG-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/385,758
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APPLICATION NUMBER: US/08/483,488
FILING DATE: 07-UN-1995
CLASSIFICATION: 55
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 5, Application US/08483488 Patent No. 5853985
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           26-AUG-1989
  Matches 266; Conservative
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PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES:
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OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: Tarrytown
STATE: New York
COUNTRY: U.S.A.
ZIP: 10591-5144
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APPLICANT: ENDEGE, WILSON O., ET AL.

TITLE OF INVENTION: ROVEL HUMAN GENES AND GENE EXPRESSION

TITLE OF INVENTION: PRODUCTS: II

FILE REFRERNCE: CCDNA_260XX

CURRENT FILING DAFE: 1999-08-30

GERLIER APPLICATION NUMBER: 05/328,111

EARLIER APPLICATION NUMBER: 60/11/393

EARLIER FILING DAFE: 1999-01-27

EARLIER FILING DAFE: 1999-01-27

EARLIER FILING DAFE: 1999-01-27

EARLIER FILING DAFE: 1999-01-27

EARLIER FILING DAFE: 1999-01-37

EARLIER FILING DAFE: 1999-01-37

SAPLIER FILING DAFE: 1999-01-37

SOFTWARE POPIL CATION NUMBER: 60/098,639

EARLIER FILING DAFE: 1999-01-37

SOFTWARE PRING DAFE: 1998-08-31

NUMBER OF SEQ ID NOS: 544
                                                                                                                                                                                                                                                                                                                                                                                                                        Score 189.4; DB 2;
Pred. No. 4.3e-25;
0; Mismatches 43;
                                                                   REFERENCE/DOCKET NUMBER: MTI 212.6-KGB TELECOMMUNICATION INFORMATION: TELECHONE: (914) 332-1700 TELEFRONE: (914) 332-1844
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; Sequence 354, Application US/09385982
; Patent No. 6262334
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OTHER INFORMATION: n = A,T,C or G
                       NAME: Kurt G. Briscoe
REGISTRATION NUMBER: 33,141
                                                                                                                                                                                                                                                                                                                                                                                                                           16.0%;
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                              INFORMATION FOR SEQ ID NO: 5
SEQUENCE CHARACTERISTICS:
LENGTH: 3804 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 16.0
Best Local Similarity 79.7
Matches 243; Conservative
                                                                                                                                                                                                                                                                         ; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-483-488-5
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                                     agtagaaaagctgcattataccacttgcttcmgttgcnttcagtgagaacgaagaaatgg
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TILLE OF INVENTION: ANTISENSE OLIGONUCLECTIDE MODULATION
TITLE OF INVENTION: OF HUMAN THYMIDYLATE SYNTHASE EXPRESSION
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ADDRESSEE: Law Offices of Jane Massey Licata
STREET: 66 East Main Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1, Application US/09089195
Patent No. 6087489
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 297.8; DB 3;
Pred. No. 6.4e-44;
0; Mismatches 2;
                                                     CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/089,195
FILING DATE: herewith
            COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-608-285A-42
; Sequence 42, Application US/09608285A
; Patent No. 6335013
; GENERAL INFORMATION:
                                                                                                                                            REGISTRATION NUMBER: 32,257
                                                                                                                                                                      TELECOMMUNICATION INFORMATION:
TELEPRONE: (609) 810-1515
TELEPRAX: (609) 810-1454
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
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Floppy disk
                                                                                                              ATTORNEY/AGENT INFORMATION: NAME: Jane Massey Licata
                                                                                                                                                          REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                               1536 base pairs
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Best Local Similarity 99.3
Matches 299; Conservative
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                                                                                                                                                                                                                                                                             Single
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Ayusawa,D.
Shimizu,K.
                                                                                                                                                                                                                                                              Nucleic Acid
                                                                                                                                                                                                                                                                                         Unknown
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PAGES: 2035-2043
DATE: 25-MAR-1985
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                                                                                                CLASSIFICATION:
                                                                                                                                                                                                                                                                            STRANDEDNESS:
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AUTHORS:
AUTHORS:
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Search completed: July 26, 2002, 16:37:26 Job time: 24120 sec

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867 15570	927	987 15690	.1047	1107	1167 15870	1227 15930	1287 15990	1347	1407	1467	1521	RESULT 13 AXO50451 LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM	REFERENCE AUTHORS TITLE JOURNAL	FEATURES SOURCE BASE COUNT ORIGIN
Qy Db	QY	QY	QY	QY	QY Db	QY	QY Db	QY	Oy Db	Qy Db	Qy Db	RES AXC LOC DEF ACC VER KEY CC	REE 7	FEP BAS ORI

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PAT 09-JAN-2
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                                                                                                                                                                                                                                Homo sapiens
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                      agactttoagattgaagggtacaatccgoatccaactattaaaqggaaatggctgttta 1046
                                                                  15510 GAACTITGITGATCACATCCTGTGTTTTCACGGACATGAGGAGCAATTACAACG 1556
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Young, P.E., Augustus, M., Carter, K.C., Ebner, R., Endress, G.,
                                                                                                                                        927 acctttcccaaagctcaggattcttcgaaaagttgagaaaattgatgacttcaaagctga
  Length 18596;
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                        Indels
                        63;
Score 613.2; DB 6;
Pred. No. 9.8e-117;
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Best Local Similarity 90.6
Matches 667; Conservative
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MEDLINE 95226450	ses Features source 279	425 CDS	485	cag 545 /product="thymidylate synthase" /protecti_id="Aab3240.1" /db_xref="Cl_1207328" /translation="MLVEGSELQSGAQQPRTEAPQHGELQYLRQVEHIMRCGFK!	605 519	665 BASE COUNT 43 ORIGIN	9tga 725 Query Match 45.4%; Score 697.8; DB 10; Length 1598 Best Local Similarity 87.7%; Pred. No. 2.4e-134; Matches 762; Conservative 0; Mismatches 107; Indels 0;	QY 181 cogcogcacggggagctgcagtacctggggcagtacctggggcagtc	119 845 241 aggaaggacgaccgcacgggcaccggcaccggtattcggcatgcaggcgcgcgc	Oy 301 agcctgagagatgaattccctctgctgacaaccaaacgtgtgttctggaagggtgttttg	aa 965 CON 361 gaggagttgctgtggtttatcaagggatccacaaatgctaaagagctgtcttccaaggga Oy 361 gaggagttgctgtgtgttatcaagggatccacaaatgctgaagagctgtcttccaaggga Oy 361 gaggagttgctgtgtgtgtgtgtgtgtgtgtgtgtggggatccacacaca	1. 1025 Qy 421 gtgaaaatctgggatgccaatggatcccgagacttttggacagctgggattctccacc	Oy 481 agagaaggacttgggcccagtttatggcttccagtggaggcattttggggcagaa	Oy 541 tacagagatatggaatcagattattcaggacagggagttgaccaactgcaaagagtgatt	AAY-2000 Qy 601 gacaccatcaaaaccatcgacgacgacagaagaatcatcatgtgcgcttggaatccaaga	Oy 661 gatcttcctctgatggcgctgcctccatgccatgccagttctatgtggtgaac	Py 721 agtgagetgtcetgccagetgtaccagagatcgggagacatgggcetcggtgtgccttcc.	
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us-09-963-333-6.rge

452 705 498

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Mus musculus, clone MGC:28246 IMAGE:3994204, mRNA, complete cds. BC020139 GI:18044896 MGC.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; M
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Contact: MGC help desk
Email: ogapbs=rémail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LiNL)
DNA Sequencing by: Baylor College of Medicine Human Genome
Sequencing Center
Center code: BCM-HGSC
Web site: http://www.hgsc.bcm.tmc.edu/cdna/
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                                   886 cacatogagocactgaaaattcagottcagogagaacccagacctttcccaaagctcagg
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Gunaratne, P.H., García, A.M., Lu,
Yoon, V.S., Kowis, C.R., Lawrence,
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VRKDDRTGTGTLSVFGMQARYSLRDEFPLLTTRRVFWRGYLEELLMFIRGSTNAKELS
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GDAHIYLNHIEPLKIQLQREPRPFPKLRILRKVEKIDDFKAEDFQIEGYNPHPTIKME
Molecular biology and Cytogenetics; 5-6-50 Shin-machi, Hino, Tokyo 191-0002, Japan (E-mail:hisatomi@srl.srl-inc.co.jp, Tel:81426483793(ex.7926), Fax:81426484043)
                                                                                                                                                                                                                                                             "Jobe" Tall alternative splicing variant The protein encoded by this gene is 34aa shorter than the full-length isoform. This variant uses an alternative splice site resulting in it lacking 102nt in the coding region compared to the full-length isoform reported in Acc#
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Pred. No. 1.2e-140;
0; Mismatches 0; Indels 102;
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/db_xref="taxon:9606"
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/cell_line="KATO III"
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X., Hulyk, S.W., Hale, S.M., S., Martin, R.G., Muzny, D.M.

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	taaagaagtgttctgc 1536			13919 1569 bp mRNA linear PRI 10-S	Homo sapiens, Similar to thymidylate synthetase, clone MGC:22884 IMAGE:4048625, mRNA, complete cds.	BC013919 BC013919.1 GI:15530266		Homo sapiens Bollo sapiens Bollo survets. Motoron. Chouldate. Commists. Wowtohants. Buttol one	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.	Strausbear Lo 1909) Strausbear Action	Direct Submission Submission Submitted (OYSEP-2011) National Institutes of Health, Mammalian Submitted (OYSEP-2011) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer	titute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2	NITH-WGC Project URL: http://mgc.nci.nih.gov Contact: WGC help desk	Email: cgapbs-r@mail.nih.gov Tissue Procurement: ATCC	CONA Library Preparation: CLONTECH Laboratories, Inc. CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)	DNA Sequencing by: Institute for Systems Biology http://www.systemsbiology.org	contact: amadan/esystemsblology.org Anup Madan, Rachel Dickhoff, Jessica Fahey, Stephanie Ford, Greene Mark Cettemen and Annuadha Madan	ene, Mark Neccentan and Andradia Madan	Clone distribution: MGC clone distribution information can be for through the I.M.A.G.B. Consortium/ILIMI at: http://image.llnl.gov	ies: irah Fiate: 31 KOW: O COLUMN: 4 s clone was selected for full length sequencing because i sed the following selection criteria: Similarity but not	identity to protein.	11569	/organism="Homo sapiens" /db_xref="taxon:9606"	/clone="MGC:12884 IMAGE:4048625" /tissue_tra="Bone marrow, chronic myelogenous leuk	/clone_lib="Nih_MGC_54" /lab_host="DH10B"	/note="Vector: pDNR-LIB" 961037	<pre>/codon_start=1 /product="Similar to thymidylate synthetase"</pre>	/protein_id="AAH13919.1" /db_xref="G1:15530267"	/translation="MPVAGSELPRRPLPPAAQERDAEPRPPHGELQYLGGIOHILRCG VRXDDRTGTGTLSVFGMOARYSLRDEFPLLTTRRVFWKGYLEELLWFIKGSTNAKELS	SKGVKIWDANGSRDFLDSLGFSTREEGDLGPVYGFQWRHFGAEYRDMESDYSGQGVDQ LORVIDFIKTNDDDRRITMCAWNDRDLDIWALDDCHALODFVVVNSFLSCOLYOPSGD	>>>===================================
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96.7%; Score 1484.6; DB 9; Length 1569; 99.3%; Pred. No. 2e-297; Live 0; Mismatches 4; Indels 6;
        arity 99.3
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DUCKES DUCKES Houns Sapiens
Homman. Homo sapiens Bukaryota, Metazoa, Bukaryota, Butheria; 1 (bases 1 to 1533; Straubberg, R. Direct Submission Submitted (05-FEB-2) Gene Collection (McG Gene Collection (McG Institute, 31 Centen USA NIH-WGC Project URL: Contact: MGC help dd Email: cgapbs-remail Tissue Procurement: CONA Library Prepare CONA Library Prepare CONA Library Prepare CONA Library Arrayed DNA Sequencing by: N Sequencing Center(Raithersburg, Maryla Reb site: DNA Library Prepare CONA Library Prepare CONACI: McDowner(Reb site: Nation of Stribution: Lim, M., Maduro, Q. L., McDowell, J., Pearson Tiongson, E.B., Touch Tiongson, E.B., Touch Tiongson, E.B., Touch Tiongson, E.B., Touch Through the I.M.A.G. Series: IRAL Plate: This clone was selec The following Location/Qu Through the I.M.A.G. Ab_Tref=""" Aba_Tref="" Aba_Tref="" Aba_Tref="" Aba_Tref="" Aba_Tref="" Aba_Tref="" Aba_Tref="" Aba_Tref="" Aba_Tref=" Aba_Tref=""
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Qy	gaggaftgctgtggtttatcaagggatccacaaatgctaaagagctgtctccaagga 	1441	Б. — Қ
QY	421 gtgaaaatctgggatgccaatggatcccgagactttttggacagcctgggattctccacc 480	Oy 1501 tgttttatatg	tgittiatatotigotataataaagaagigitotgo 1536
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QY	601 gacaccatcaaaaccaacctgacgacagaagaatcatcatgtgcgcttggaatccaaga 660 		ens ; Metazoa; Chordata; Craniata; Vertebrata; Euteleostom. Eutheria; Primates; Catarrhini; Hominidae; Homo.
QY Dp	661 gatcttcctctgatggggctgcctccatgccatgccctctgccagttctatgtggtgaac 720	REFERNCE 1 (bases AUTHORS Takeishi, Seno,T. TITLE Nucleotid	<pre>1 (bases 1 to 1>36) Takeishi,K., Kaneda,S., Ayusawa,D., Shimizu,K., Gotoh,O. and Seno,T. Nucleotide sequence of a functional cDNA for human thymidylate</pre>
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Qy	781 aacatcgocagctacgccctgctcacgtacatgattgcgcacatcacgggcctgaagcca 840	ω.	Location/Qualifiers 1, .1536 1d_zraf="Homo sapiens" /db_zref="taxon:9606"
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was primed with a NotI-oligo(dT) primer. Five prime end
enriched, double-stranded cDNA was digested with Not I and
cloned into the Not I and Eco RV sites of the pCMVSPORT 6
vector. Library is not normalized, but is the control for
the normalized libraries. Library was constructed by Life
Technologies. Contact: Feng Liang Life Technologies,
division of Invitrogen 9800 Medical Center Drive Rockville
, Maryland 20850, USA Fax: (1) 301 610 8371 Email:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     923 bp mRNA linear EST 13-FEB-2001
Homo sapiens cDNA clone CS0DA001XD20 3
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Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
Unpublished (2001)
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Email: segref@genoscope.cns.fr, Web
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Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches 915; Conservative
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/ussue_type_traducts
/note="Vector: pCwNSpORT 6; Site_1: Not1; 1st strand ob
was primed with a Not1-ol1go(dT) primer. Five prime en-
enriched, double-stranded cDNA was digested with Not I.
cloned into the Not I and Eco RV sites of the pCMNSpORT
vector. Library was normalized. Library was constructed
Life Pechnologies. Context: Fend Lings Lie Technologi-
a division of Invitrogen 9800 Medical Center Drive
Rockville, Maryland 20850, USA Fax: (1) 301 610 8371
Email: fliang@ilfetech.com URL.
http://fullength.invitrogen.com."

http://fullength.invitrogen.com."
20 a 263 c 254 g 193 t 2 others
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Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished (2001)
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVPX cedex - France
Email: seqrefégenoscope.cns.ir, Web : www.genosc
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Pred. No. 5.7e-192;
1; Mismatches 2;
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gcacgggcaccggcacctgtcggtattcggcatgcaggcgctacagcctgagagatg 313	aattocototgotgacaaccaaacgtgtgttotggaagggtgttttggaggagttgctgt 373	ggtttatcaagggatccacaaatgctaaagagctgtcttccaagggagtgaaaatctggg 433	atgccaatggatcccgagactttttggacagcctgggattctccaccagagaagaaggg 493	acttgggcccagtttatggcttccagtggaggcattttggggcagaatacagagatatgg 553	aatcagattattcaggacagggagttgaccaactgcaaggagtgattgacaccatcaaaa 613	ccaaccctgacgacagaagaatcatcatgtgcgcttggaatccaagagatcttcctctga 673	tggcgctgcctccatgccatgccctctgccagttctatgtggtgaacagtgagctgtct 733	gccagctgtaccagagatcgggagacatgggcctcggtgtgcctttcaacatcgccagct 793	acgccctgctcacgtacatgattgcgcacatcacgggcctgaagccaggtgactttatac 853	acactttgggagatgcacatatttacctgaatcacatcgagccactgaaattcagcttc 913	agogagaaccagaactttccaaagctcagg 945	AL515911 SM AL515911 SM AL515911 SM AL515911 SM Homo sapiens cDNA clone CsODA001YD20 5 AL515911.1 GI:12779404 EST 13-PEB-2001 AL515911 GI:12779404 EST 13-PEB-2001 AL515911 AL515911 SM Homo sapiens ENARTYCA: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. ENARTYCA: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. ENARTYCA: Aloses 1 to 955 I. 10 WB. Gruber, C. Jessee, J. and Polayes, D. Full-length cDNA libraries and normalization Contact: Genoscope Genoscope - Centre National de Sequencage BP 191 91006 ENRY cedex - France EMB 191 91001
Qy 254	Qy 314	Qy 374	Oy 434	Qy 494	Qy 554	Oy 614	Qy 674	Qy 734	Qy 794	Qy 854	Qy 914	RESULT 9 AL515911 LOCUS DEFINITION VERSION VERSION VERSION VERSION TOTALE ORGANISM TITLE JOURNAL COMMENT FEATURES SOURCE
Db 247	Db 307	Db 367	Db 427	Db 487	Db 547	Db 607	Db 667	Db 727	Db 787	Db 847	Db 907	

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/note-"Organ: brain; Vector: pCMVSPORT 6; 1st strand cl was primed with a NotI-oligo(dT) primer. Five prime encenriched, double-stranded bnNa was digested with Not I cloned into the Not I and Eco RV sites of the pCMVSPORY vector. Library is not normalized, but is the control the normalized libraries. Library was constructed by Li Technologies. Contact: Fong Library was constructed by Li Technologies. Contact: Fong Liang Life Technologies, division of Invitrogen 9800 Medical Center Drive Rockvi Maryland 20850, USA Fax: (1) 301 610 8371 Email: fliang@lifetech.com URL: http://fulllength.invitrogen.com" 9 others
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Pred. No. 1.7e-197;
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98.1%;
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Matches 977; Conservative
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostom Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 935)
Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length DNA libraries and normalization
Unpublished (2001)
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AL542409
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BP 191 91006 EVRY cedex - France
Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
                                                                                                                                                                                                                                                                                                              860 t-gggagatgcacatatttacctgaatcacatcgagccactgaaaattcagcttcagcga
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/tissue_type="Placenta"
/t
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
Unpublished (2001)
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Pred. No. 6.2e-200;
7; Mismatches 4;
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/db_xref="taxon:9606"
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                                               1488 tgaactttaAagttgttttatatg 1511
                                                                      24 TGAACTTTAAAGTTATAGTTGTTG 1
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Best Local Similarity 98.6'
Matches 966; Conservative
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Eutelecstomi Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo. 1 (bases 1 to 1020) Li,W.B., Gruber,C., Jessee,J. and Polayes,D. Full-length cDNA libraries and normalization Unpublished (2001)

GI:12881832

AL547612.1

ACCESSION VERSION

KEYWORDS

Homo sapiens

ORGANISM

JOURNAL

TITLE

REFERENCE AUTHORS

human

prime, mRNA sequence. AL547612

Genoscope - Centre National de Sequencage BP 191 91006 EVRY cedex - France Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr.

/organism="Homo sapiens" /db_xref="taxon:9606" /clone="CS0DI008YH21

Location/Qualifiers

FEATURES

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ggctgtttagggtgctttcaaaggagctCgaaggatattgtcagtctttaggggttgggc 1097
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gggcccagtttatggcttccagtggaggcattttggggcagaatacagagatatggaatc 557
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                                                                                        coctgacgacagaagaatcatcatcatgtgcgctttggaatccaagagatcttcctctgatggc
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                                             agattattcaggacagggagttgaccaactgcaaagagtgattgacaccatcaaaaccaa
                                                                                                               CCCTGACGACAGAATCATCATCATGTGCGCTTGGAATCCAAGAGATCTTCCTCTGATGGC
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237

BASE COUNT ORIGIN

/clone_lib="LTL_NFL006_PI2"
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/tissue_type="placenta"
/note="Vector: prowysporr 6; Site_1: NotI; 1st strand cD
was primed with a NotI-oligo(dI) primer. Five prime en
enriched, double-stranded cDNA was digested with Not I
cloned into the Not I and ECO RV sites of the priMSPORT
vector. Library was normalized. Library was constructed
Life Technologies. Contact: Feng Library was constructed
Library./fulllength.nnvitrogen.com URL:
Library./fulllength.nnvitrogen.com
Library./fullength.nnvitrogen.com
Library./fullength.nnvitrogen

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tecaacacatecteegetgeggegteaggaaggaegaeegeaegggeaeeggtaeetgt
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                                                                                          aacgtgtgttctggaagggtgttttggaggagttgctgtggtttatcaagggatccacaa
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                   ő
Length 1020;
                   Indels
Score 1018; DB 9;
Pred. No. 1.2e-218;
1; Mismatches 1;
 66.3%;
99.8%;
                     Conservative
          Similarity
                     Matches 1018;
  Query Match
Best Local 9
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120

154

9 46

Gaps

180 274 240 334 300 394 360 454 420 480

DEFINITION

RESULT A

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This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 10835001 This clone has the following problem: no 5' EST match. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                    712
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                tgaagccaggtgactttatacacactttgggagatgcacatatttacctgaatcacatcg 892
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                                                                                                                                                                                                                                                                                                                                  agccgcgtccgccgcacggggggggctgcagtacctgggggcagatccaaccatcctccgct 232
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/db_xref="taxon:9606"
/clone="IwAGE:31414119"
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/lab_host="DH10B-R"
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Pred. No. 0;
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Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
GAAAAGTIGAGAAAATIGAGACTICAAAGCTGAAGACTICAGATIGAAGGGAACATC
                                                                                                                                                                                                          gaaGaaggaactaggtcaaaaatctgtccgtgacctatcagttattaattttaaggatg
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Li.W.B., Gruber.C., Jessee,J. and Polayes,D.
Hill-length convalibraties and normalization
Unpublished (2001)
Contact: Genoscope
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/clone="CSODIO61YF09"
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The present invention describes colon tumour associated proteins (I) and (II) and (II) and be used in gene therapy and vaccine production. (I) and (II) and be used in gene therapy and vaccine production. (I) and (II) may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate colon tumour associated protein (TCAP) expression, such as colonic cancer. For example, (I) and (II) may be used to treat disorders associated with decreased expression by rectifying mutations or deletions in a patient's genome that affect the activity of TCARP by expressing inactive proteins or to supplement the patients own production of them. Additionally, (II) may be used to patients own production of them. Additionally, (II) may be used to patients own production of them. Additionally, (II) may be used to complementary sequences may also be used as DNA probes in diagnostic complementary sequences may also be used as DNA probes in diagnostic polymerase chain reaction (PCR) and hybridisation assays to detect and quantitate the presence of similar nucleic acids in samples, and in assays to identify modulators of TCAP expression and activity. The anti-(I) antibodies and antagonists may also be used to down regulate as diagnostic agents for detecting the presence of TCAP expression and activity. The anti-(I) antibodies and antagonists may also be used to down regulate as diagnostic agents for detecting the presence of TCAPs in samples and antagonists may also be used to down and antagonists and antagonists may also be used as diagnostic agents for detecting the presence of TCAPs in samples and antagonists may also be used as diagnostic agents for detecting the presence of TCAPs in samples and AAM24521 represent nucleotide and amino acid sequences given in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Colon tumor associated proteins and nucleic acids useful for the prevention, diagnosis and treatment of colonic cancer -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Secrist H, Benson DR, Meagher MJ, Stolk JA;
immunogenic; gene therapy; vaccine; colonic cancer; ss.
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11-FEB-2000; 2000US-054629.
06-MAR-2000; 2000US-051444.
19-MAY-2000; 2000US-057251.
29-JUN-2000; 2000US-069448.
                                                                                                                                                                                            29-DEC-2000; 2000WO-US35596.
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King GE, Wang T, Jiang Y;
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                                                                                            WO200149716-A2.
                                                Homo sapiens.
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        Qy
        1187 aggatgttgccactggcaatgtaactgtgccagttcttccataataaaaggctttgag
        1246

        Db
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        107

        Qy
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        Db
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        47

        Qy
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        1352

        Db
        46 GTATGTGCTCTTAGCAAAACATGTATGCAATTCAATCCCACGT
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Search completed: July 26, 2002, 17:57:13 Job time: 12327 sec developmental biology; cell signalling; insecticide;

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Myers EW;

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Drosophila melanogaster expressed polynucleotide SEQ ID NO 11765.
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                                                                     Length 2966;
                                                                                                                       9;
                                                                                                                       Indels
Sequence 2966 BP; 808 A; 640 C; 664 G; 854 T; 0 other;
                                                                   Score 383.8; DB 23;
Pred. No. 7e-90;
0; Mismatches 292;
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                                                                     25.0%;
65.9%;
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ID ABLC
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AC ABLC
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The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher euksayotes for the development of insclicides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABLi6176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPM at ftp.wipo.int/pub/published_pct_sequences.
                                                                                        isolated nucleic acid detection reagent for detecting 1000 or mores from Drosophila and for elucidating cell signalling and cell-cel.
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                                                                                                                                                                                                                                       claim 1; SEQ ID NO 11765; 21pp + Sequence Listing; English.
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Pred. No. 4.5e-89;
0; Mismatches 287;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 24.7%;
Best Local Similarity 66.0%;
Matches 568; Conservative
WPI; 2001-656860/75.
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                                 P-PSDB; ABB61658
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Location/Qualifiers

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Key
                                         20663 GCGCACAGAAGGAGGGGGATTTGGGACCTGTTTACGGTTTCCAGTGGAGGCACTTTGGG 20604
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              295 cgctacagcctgagagatgaattccctctgctgacaaccaaacgtgtgttctggaagggt 354
                                                                                                         355 gittiggaggagtigcigiggittaicaagggaiccacaaaigctaaagagcigicticc 414
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interleukin-6; IL-6; interferon regulatory factor; rheumatoid arthritis; complement-binding protein; glycoprotein; capsid protein IV; infection; immediate early protein; Raposis sarcoma; protective vaccine; lymphoma; HIWphoproliferative disease; leukaemia; splenomegaly; mycosis fungoides; HIV immune status; anti-inflammatory agent; therapy; ds.
                                                                                                                                                                                                      KSHV; HHV8; human herpes virus 8; macrophage inflammatory protein II;
                                                                                                                                                           KSHV long unique coding region and terminal repeat.
                                                                                                                                                                                                                                                                                                                                               Kaposi's sarcoma-associated herpes virus.
                                      AAV19941 standard; DNA; 137507 BP
                                                                                                                   03-AUG-1998 (first entry)
                                                                            AAV19941;
RESULT 11
AAV19941/C
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New nucleic acid encoding Kaposi's sarcoma associated herpes virus proteins - useful for, e.g. detecting levels of HHV8 in, and preparation of vaccines for treatment of, HIV patients
                                                                                                              /product= macrophage inflammatory protein II complement (27137..27424)
                                                                                                                                     /product= interferon regulatory factor 1
28661..29741
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                                                                                                                                                                                                                                                              /product= interferon regulatory factor 2 89600..90541
                                                                                                                                                                                                                                                                                           /product= interferon regulatory factor 3
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                           /product= complement-binding protein
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                                                        /product= glycoprotein B complement (17261..17875)
                                                                                     /product= interleukin 6
complement (21548..21832)
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complement (58976..60175)
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                                                                                                                                                                                                                                                                                                                          /product= glycoprotein X complement (93636..94127)
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25-JUL-1996;
25-JUL-1996;
25-JUL-1996;
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encoded by the genome sequence. The present invention also specifically claims the individual open reading frame (ORF) nucleotide sequences from the genome which encode the individual proteins, but these sequences are not given. A non-human animal infected with RRV can be used for testing the efficacy of drug in the treatment of condition associated with infection with RRV such as Kaposi's sarcoma, lymphoproliferative
                                                                                                                                                                                                                                        disorders, B-cell hyperplasia, lymphadenopathy, spenomegaly, hypergammaglobinulinaemia or autoimmune haemolytic anaemia, by administering the drug to a immuno-compromised non-human primate preferably Rhesus macaque monkey obtained by as a result of infection by Simian Immunodeficiency Virus (SIV). RRV is useful for producing non-human primate model for testing potential treatments for conditions associated with RRV infection. It is also useful for testing the efficacy of the candidate vaccine against RRV infection or conditions associated with its infection by administering the vaccine to the subject capable of infection with RRV, incomlating the subject with RRV and observing the effect of vaccine. AAG64755 to AAG64765 and AAB53205 to AAB53213 represent sequence used in the exemplification of the
macaca mulatta rhadinovirus 17577 (RRV). AAC64754 represents the
                             genome sequence, and AAB53123 to AAB53204 represent the proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        present invention.
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Sequence 133719 BP; 32746 A; 35648 C; 34521 G; 30804 T; 0 other;

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                                                                                                                    21637 CACGGCGAGCTGCAGTACTTGGCGCACCTGGATTTAATTATTAAACACGGCGTGCAGAGG 21578
                                                                                                                                                                                      11097 CTGTCCTGCCAGCTGTACCAGAGGTCCGCCGACATGGGCCTCGGGGTCCCGGTTAACATC 21038
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                                                                             187 cacgggggagctgcagtacctgggggcagatccaacactcctccgctgcggcgtcaggaag 246
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Score 404.6; DB 21; Length 133719;
                                          0
                                        Indels
                  Pred. No. 1.7e-94;
0; Mismatches 284;
26.3%;
66.9%;
              Best Local Similarity 66.9
Matches 575; Conservative
  Query Match
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macrophage inhibitory protein (vMIP)-1A and -1B and beta-chemokine-like (BCK) protein. The sequences of these proteins are given in AAM40100-W40100-W40100.

Polynucleotide containing HHV-8 genes encoding one or more of these proteins. The invention also claims that the polynucleotide and the proteins. The invention also claims that the polynucleotide and the proteins are to diagnose an HHV-8 associated disease, e.g. using antibodies to the proteins, to diagnose an HILiple myelome and body cavity based large cell lymphoma (BCBL). The proteins have also been claimed to be

compounds for drugs to treat HHV-8 diseases.

useful in screening

Sequence 1014 BP; 216 A; 239 C; 286 G; 273 T; 0 other;

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20977 TITGIGCACACCIIGGGGACGCCCACGIITACAACAACCACGIIGAICCCCIGCIGCII 2091:
                                                                                                                                                     20857 cregaegacriracecececedarcreacrerceaegecraceacececarcceacara 2079
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (HHV'8) divergent locus DL-B which lies between open reading frames 11 and 17. Sequencing of the HHV-8 divergent locus DL-B revealed the presence of nine viral ORRS with gene products related to cellular proteins. These proteins include the thymidylate synthase (TS), dihydrofolate reductase (DHFR), Bcl-2 homologue, IE-1A, IE-IB and, four cytokines which include viral interleukin-6 (vIL-6), viral
                                                                                                                        967 attgatgacttcaaagctgaagactttcagattgaagggtacaatccgcatccaactatt 1026
                                                        cagottoagogagaaccoagacotttocoaaagotcaggattottogaaaagttgagaaa 966
847 tttatacacactttgggagatgcacatatttacctgaatcacatcgagccactgaaaatt 906
                                                                                                                                                                                                                                                                                                                                                                                                                      DL-B; thymidylate synthase; dihydrofolate reductase; probe; HHV-8; Bcl-2 homologue; IE-1A; IE-1B; viral macrophage inhibitory protein; Kaposi's sarcoma; beta-chemokine-like; hydridisation; vIL-6; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New human herpes virus gene region containing 8 open reading frames - useful for, e.g. diagnosing Kaposi's sarcoma or body cavity based
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                                                                                                                                                                                                                                                                                                                                                                                           Human herpesvirus 8 (HHV-8) divergent locus DL-B probe 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hardwick JM, Hayward GS, Nicholas J, Reitz MR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Kaposi's sarcoma associated herpesvirus.
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                                                                                                                                                                                                                   20797 GAGATGGAGATGGCCGTTT 20779
                                                                                                                                                                                       1027 aaaatggaaatggctgttt 1045.
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The present sequence represents the nucleotide sequence of Varicella virus, Dumas strain. The specification describes a method for the quality control of an attenuated pox vaccine, characterised in that the DNA sequence of specific parts of the viral genome in a sample is determined and proved to be conserved rather than mutated in comparison
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actgtgccagttctttccataataaaggctttgagttaactcactgagggtatctgaca
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                                                                                                                                       tgagtaacaccatcgatcatgatgtagagtgtggttatgaactttaAagttgttttatat
                                                                                                                                                                                                                                 Dumas strain; pox vaccine; vaccine; poxvirus disease; chickenpox;
                                                          241 actgtgccagttctttccataataaaaggctttgagttaactcactgagggtatctgaca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      with the same parts of a reference viral genome. The method is for quality control of vaccines for use in the prevention of po
                                                                                                                                                                                                                                                                                                                                                                                                                      Nucleotide sequence of the Varicella virus Dumas strain
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                                                                                                                                                                                                                                                                    gttgctataataaagaagtgttctgc 1536
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Sequence 124884 BP; 33789 A; 29295 C; 28177 G; 33623 T; 0 other;

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18848 ctgtcaatcaaactatttacagcaaggaatcgatcagctgcaaactgttatagatacaat 1890
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Length 124884;
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Score 408; DB 22;
Pred. No. 2.1e-95;
0; Mismatches 295;
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   26.6%;
66.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present invention relates to a method for assaying an analyte in a sample comprising; contacting the sample with a mutant analyte-binding enzyme which has binding affinity for the analyte or an immediate analyte enzymatic conversion product but has attenuated catalytic activity; and detecting resulting binding. The method is useful in monitoring biological systems/processes, or prognosis/diagnosis of disease caused by imbalances of the analytes. The present sequence is a coding sequence used in the present invention.

Note: the present sequence is not shown in the specification, but was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          agactttcagattgaagggtacaatccgcatccaactattaaaatggaaatggctgttta 1046
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Assaying method, useful for prognosis and diagnosis of disease, comprises contacting sample with a mutant analyte-binding enzyme and detecting binding -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    39.9%; Score 613.2; DB 22; Length 18596; 90.6%; Pred. No. 2e-149; Live 0; Mismatches 63; Indels 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           from Genbank, using information given in the specification.
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                                                                                                                                                                                                                                                       Analyte-binding enzyme; analyte analysis; ss.
                                                                                                                                                                                                                        Thymidylate synthase coding sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; Page -; 187pp; English.
                                                                                                                            AAF31109 standard; cDNA; 18596 BP
                                                                                                                                                                                                                                                                                                                                                                               30-JUN-2000; 2000WO-US18057
                                                                                                                                                                                                                                                                                                                                                                                                            99US-0347878
99US-0457205
                                                                                                                                                                                          (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            (GEAT ) GEN ATOMICS
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                                                GTTCTGC
                                                                                                                                                                                                                                                                                       Homo sapiens,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; schizophrenia; developmental disorder; spina bifida cystica; Tourette's syndrome; bipolar illness; autism; conduct disorder; attention deficit disorder; obsessive compulsive disorder; chronic multiple tic syndrome; learning disorder; polymorphism; ds.
                                                                                                                                                                                                                                                                                        Human thymidylate synthase gene SEQ ID NO: 11.
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                                                             sequences that are differentially expressed during foam cell differentiation. The polynucleotide sequences of the invention or a composition comprising these polynucleotides are useful as a high throughput method for detecting altered expression of one or more polynucleotides in a sample. The polynucleotides can be used in the diagnosis of disorders associated with foam cell development such as atherosclerosis, cerebral stroke, and cardiovascular disorders such as coronary artery disease. The polynucleotide sequences can also be used as PCR primars and probes. The polynucleotide sequences can also be used useful in gene therapy. Assign 18.85.95.21 represent the human polynucleotide sequences of the invention are also polynucleotide sequences of the invention are also
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                                                    present invention relates to the isolation of human
                                                                                                                                                                                                                                       Sequence 3298 BP; 898 A; 709 C; 744 G; 919 T; 28 other;
are differentially expressed in foam cell development
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                                                                                                                                                                                                                                                                              97.3%; Score 1494.8;
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0; Mismatches
                           English
                                                                                                                                                                                                                                                                                                                                               Page 250-251; 315pp;
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medical imaging; diagnostic; genetic disorder;
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GENERAL INFORMATION:
APPLICANT: Schaffer, Priscilla A.
APPLICANT: 111y
TILLE OF INVENTION: Compositions and Methods for Treatment of Herpesvir TILLE OF INVENTION: Infections
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock, Washburn, Kurtz, Mackiewicz & No. 5821339ris
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 70 ccacttcgcctgcctccqcccgcccgccgccgccatgcctgtggccggctcggagctg 129
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STREET: One Liberty Place, 46th floor
CITY: Philadelphia
                                                                                                                                                                                                                                                                                                                                                                                                        Score 48.6; DB 4; Length 1292; Pred. No. 0.002; 0; Mismatches 84; Indels 0
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APPLICATION NUMBER: US/08/458,568A
FILING DATE: 02-010E-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 08/065,146
FILING DATE: 05-MAY-1993
CLASSIFICATION: 435
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COUNTRY: USA
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Ploppy disk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 3, Application US/08458568A Patent No. 5821339
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NAME: Leary Ph.D., Kathryn R.
REGISTRATION NUMBER: 36,317
                                                                                                                                                                                                                                                                           MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                               3.2%;
      TELEFAX: 312/474-0448
TELEX: 25-3856
INFORMATION FOR SEG ID NO: 37
SEQUENCE CHARACTERISTICS:
LENGTH: 1292 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
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TELEPAX: (215) 568-3439
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 702 base pairs
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Best Local Similarity 54.11
Matches 99; Conservative
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US-08-458-568A-3/c
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APPLICANT: Chou, Joany
TUTLE OF INVENTION: Method For Treating Tumorigenic Diseases
TUTLE OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
                                                                                                                                                                                                                                                                                                                                                                                                        Score 48.6; DB 4; Length 1292;
Pred. No. 0.002;
0; Mismatches 84; Indels 0
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APPLICATION NUMBER: US/09/283,471A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Zeller, James P.
REGISTRATION NUMBER: 28,491
REFERENCE/DOCKET NUMBER: 27373/32742A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STATE: Illinois
COUNTRY: United States of America
ZIP: 06060-640.
COMPUTER READABLE FORM:
MEDIUM IYPE: Floppy disk
COMPUTER: IBW PC COMPATIBLE
OPERATING SYSTEM: PC-POS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 04 APR-1999
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 37, Application US/09283471A Patent No. 6340673 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 31-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/419,853
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: 07/861,233
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                                                                                                                                                                                                                                                                    ; MOLECULE TYPE: DNA (genomic)
US-08-483-533-37
                                                                                                                                                                                                                                                                                                                                                                                                        3.2%;
TELEFAX: 312/474-0448
TELEX: 25-3866
INFORMATION FOR SEQ ID NO: 37
SEQUENCE CHARACTERISTICS:
EMOTH: 1292 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 11-APR-1995
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ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 54.18
Matches 99; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION: 514
PRIOR APPLICATION DATA:
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APPLICATION NUMBER: (
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US-09-283-471A-37
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1608 TATICAAATCATATTGATGCGATKCGMAACACCATTAGCACGTGAAAGCTTCAATCCTCC 1549
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                                                              877 tacctgaatcacatcgagccactgaaaattcagcttcagcgagaacccagacctttccca 936
                                                                                                                                                aageteaggattettegaaaagttgagaaaattgatgaetteaaagetgaagaettt-ca 995
                                                                                                                                                                                                                                                             996 gattgaagggtacaatccgcatccaactattaaaatggaaatggctgtttag 1047
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Sun, Dongxu
TITLE OF INVENTION: METHODS OF SCREENING FOR COMPOUNDS
TITLE OF INVENTION: ACTIVE ON STAPHYLOCOCCUS AUREUS
TITLE OF INVENTION: TARGET GENES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: September 13, 1996
APPLICATION NUMBER: 60/009,102
FILING DATE: December 22, 1995
APPLICATION NUMBER: 60/003,798
FILING DATE: September 15, 1995
ATTONEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US/09/266,417
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TELECOMMUTICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA: APPLICATION NUMBER: 08/714,918
                                                                                                                                                                                                                                                                                                                                                                                   Sequence 7, Application US/09266417 Patent No. 6228588
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633 West Fifth Street
Suite 4700
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Malouin, Francois
Martin, Patrick K.
Schmid, Molly B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM Compatible OPERATING SYSTEM: IBM P.C. SOFTWARE: Word Perfect 5.1 CURRENT APPLICATION DATA:
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FILLING DATE: March 9, 1999
CLASSIFICATION: 435
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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EDNESS: single
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Ly
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STATE: California
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APPLICANT:
APPLICANT:
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US-09-266-417-7
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APPLICANT:
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1728 ATAICITITIAGGIGIGCCATITAATAICGCARGCIACGCITIAITGACACACCTIAIIG 1669
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                                                                                                                                                                        teatgigegetiggaatecaagagatetteetetgaiggegetgeeteeatgeee 697
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                                                                                   tetgecagitetatgiggigaacagigageigiecigecageigiaecagagaieg
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STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Roizman, Bernard
APPLICANT: Chou, Joany
TITLE OF INVENTION: Method for Treating Tumorigenic
TITLE OF FUNDENTION: Diseases
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                             6; Mismatches 194;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REGISTRATION NUMBER: 28,491
REFERENCE/DOCKET NUMBER: 28097/32742
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STATE: Illinois
COUNTRY: United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/483,533
FILING DATE: 07-MAR-95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/419,853
FILING DATE: 11-APR-95
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    7.9%;
56.8%;
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 31-MAR-92 ATTORNEY/AGENT INFORMATION:
                                               Matches 268; Conservative
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PRIOR APPLICATION DATA:
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      Query Match
Best Local Similarity
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                                                                                                                                                                             638
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20243 CCACTACGGCTGCAGCTGACGCGCACTCCACGTCCCTTTCCGCGCCTGGAGATACTCCGG 20184
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20483 CCGCCGACTTGTCGTTGATGGCGCTTCCGCCCTGTCACTTGTTATGTCAATTTTATGTA
                                                                                                                                                                                  775 cettteaacategecagetacgecetgeteacgtacatgattgegeacateacgggeetg
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APPLICANT: Malouin, Francois
APPLICANT: Malouin, Francois
APPLICANT: Martin, Patrick K.
APPLICANT: Schmid, Wolly B.
APPLICANT: Sun, Dongxu
APPLICANT: Sun, Dongxu
TITLE OF INVENTION: STAPHYLOCOCCUS AURBUS ANTIBACTERIAL
TITLE OF INVENTION: TARGET GENES
CORRESPONDENCES: 111
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20123 CATCCTACCATTCGTATGGAAATGGCAGTATAG 20091
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1015 catccaactattaaaatggaaatggctgtttag 1047
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COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM COMPATIBLE OPERATING SYSTEM: IBM P.C. DOS 5.0 SOFTWARE: Word Perfect 5.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/714,918
FILING DATE: September 13, 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 222/005
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 45R-0410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: September 13, 1996
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/009,102
FILING DATE: December 22, 1995
APPLICATION NUMBER: 60/003,798
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: September 15, 1995 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 7, Application US/08714918
Patent No. 6037123
GENERAL INFORMATION:
APPLICANT: Benton, Bret
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Warburg, Richard J. REGISTRATION NUMBER: 32,3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: Los Angeles
STATE: California
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1908 TIGATCAACTTAAAACAGTAATTGAACAAATTAAGCATAATCCAGATTCAAGGCGACACA 1849
                                                                                                                                                                                                                                                                                                                     1848 regrarecargeaarceaacagaaarrearacaargecacrrececcrrercaracca 1789
                                                                                                                                                                                                                                                                                                                                                                          tacctgaatcacatcgagccactgaaaattcagcttcagcgagaacccagacctttccca 936
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        818 egeacateacg-ggcetgaagecaggtgaetttatacacaetttgggagatgcacatatt 876
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            aagotcaaggattottogaaaagttgagaaaattgatgacttcaaagotgaagacttt-ca 995
                                                                                                                                                                                                                                                                                       638 toatgigogottiggaatocaagagatottoctotigatggogotgootcoatgocatgooc 697
                                                                                                                                                                                                                                                                                                                                                     tctgccagttctatgtggtgaacagtgagtgtcctgccagctgtaccagagatcgggag 757
                                                                                                                                                                                                                                                                                                                                                                                                                       758 acatgggcctcggtgtgcctttcaacatcgccagctacgccctgctcacgtacatgattg 817
                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 3479;
                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Sun, Dongxu
TITLE OF INVENTION: MCHHODS OF SCREENING FOR COMPOUNDS
TITLE OF INVENTION: ACTIVE ON STAPHYLOCOCCUS AUREUS
TITLE OF INVENTION: TARGET GENES
NUMBER OF SEQUENCES: 111
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
                                                                                                                                                       Score 121.2; DB 3;
Pred. No. 1.7e-22;
6; Mismatches 194;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 7, Application US/09265315 Patent No. 6187541
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Lee, Ving J.
APPLICANT: Malouin, Francois
APPLICANT: Martin, Patrick K.
APPLICANT: Schmid, Molly B.
                                                                                                                                                            7.9%;
          INFORMATION FOR SEQ ID NO: 7
SEQUENCE CHARACTERISTICS:
LENGTH: 3479 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                              Query Match 7.9
Best Local Similarity 56.8
Matches 268; Conservative
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APPLICANT: Benton, Bret
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STATE: California
COUNTRY: U.S.A.
                                                                                            ; TOPOLOGY: linear
US-08-714-918-7
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67-3510
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US-09-265-315-7/C
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TELEPHONE: (212) 278-0400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
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ZIP: 10036
COMPUTER READABLE FORM:
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: U.S.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 5
US-08-757-669A-17/C
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STREET: 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20903 GGCAGCGATCGACTCGACCGCATAGGCACCTCTCTCTATTTGGCATGCAGGCC 20844
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        20723 ACAGGAGICAAGAIAIGGGACAAAAIGGCICCAGGGAGIICCIGGCCGGGCGCGGGCTIG 20664
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21023 GGCGTCTTGGCCTTTGGCCCCCGAGGTTGACCCTTGTTCGATTCAGCATGAGGTAACTGGG 20964
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                                   APPLICANT: Bohenzky, Roy A.
APPLICANT: Russo, James J.
APPLICANT: Russo, James J.
APPLICANT: Relman, Isidore S.
APPLICANT: Moore, Parlick S.
TITLE OF INVENTION: POLYPEPFIDES FROM KAPOSI'S SARCOMA-ASSOCIATED
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 387.4; DB 2;
Pred. No. 1.1e-92;
0; Mismatches 341;
                                                                                                                                                                                                     SEE: Cooper & Dunham LLP: 1185 Avenue of the Americas New York
                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/08/770,379
                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REGIENKATLUN NORDLAND.

REFERRNCE/DOCKET NUMBER: 52342
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 278-040
TELEFAX: (212) 391-0225
INFORMATION POR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 35100 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORREY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: DNA (genomic)
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MEDIUM TYPE: Floppy disk
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Best Local Similarity 63.5
Matches 592; Conservative
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                    APPLICANT: Chang, Yuan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: 435
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear
                                                                                                                                                                                                                                                               New York
                                                                                                                                                                                                                                                                                  U.S.A.
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRANDEDNESS:
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                                                                                                                                                                                                                                                                                COUNTRY: U ZIP: 10036
                                                                                                                                                                                                       ADDRESSEE:
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20183 TCTGTTTCTTCCATGGAAGAGTTTACACCTGATGATTTTAGACTGGTGGACTACTGCCCG 2012
20423 GCTGACGGTGAGCTTTCCTGTCAGCTGTATCAGAGGTCGGGAGACATGGGTTTGGGAGTT 2036
                                                                                                                                                                                                                                                                                                                                                                                                                                          20363 CCTITIAACATIGCCAGCTATICCCICTTAACTIATATGCTIGCTCATGTTACTGGFCTT 2030
                                                                                                                                                                                                                                       20303 AGACCCGGGGGGTTTATTCACACGTTGGGAGATGCCCACATCTACAAAACGCATATAGAG 2024
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                                                                       gtgattgacaccatcaaaaccaaccctgacgacagaagaatcatcatgtgcgcttggaat 654
                                                                                                                                                                                    gigaacagigagcigiccigccagcigiaccagagaicgggagacaigggccicggigig 774
                                                                                                                                                                                                                                                                                                                                                                                                        cettteaacategecagetaegecetgeteaegtaeatgattgegeacateaegggeetg 834
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APPLICANT: Russo, James J.
APPLICANT: Rallann, Isidore S.
APPLICANT: Moore, Patrick S.
APPLICANT: Moore, Patrick S.
TITLE OF INVENTION: UNIQUE ASSOCIATED KAPOSI'S SARCOMA VIRUS TITLE OF INVENTION: SOGUENCES AND USES THEREOF NUMBER OF SEQUENCES: 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Patentin Release #1.0, Version #1.30
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1185 Avenue of the Americas
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APPLICATION NUMBER: US/08/757,669A
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 17, Application US/08757669A Patent No. 6183751 GENERAL INFORMATION: APPLICANT: Chang, Yuan
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1320

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PREVENTING, AND TREATING
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           GAGAAAATTGATGATGACTCGAAAGCTGAAGACTTTCAGATTGAAGGGTACAATCGGCATCCA
                                         actattaaaatggaaatggctgtttagggtgctttcaaaggagctCgaaggatattgtca
                                                                                                      GICTITAGGGGGTIGGGCIGGAIGCCGAGGTAAAAGTICTITITGCICTAAAAAAGG
                                                                                                                                                                       ggcaaatgtaactgtgccagttcttccataataaaaggctttgagttaactcactgagg
                                                                                                                                                                                   caaaaacatgtatgtgcatttcaatcccacgtacttataaagaaggttggtgaatttcac
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                39.9%; Score 613.2; DB 4; 90.6%; Pred. No. 8.3e-153;
                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Johnson, William G.
APPLICANT: Stenroos, Edward S.
TITLE OF INVENTION: METHODS FOR DIAGNOSING,
TITLE OF INVENTION: DEVELOPMENTAL DISORDERS
FILE REFERENCE: 601-1-057
CURRENT APPLICATION NUMBER: US/09/318,448
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NUMBER OF SEQ ID NOS: 46
SOFTWARE: PatentIn Ver. 2.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-318-448-11; Sequence 11, Application; Patent No. 6210950; GENERAL INFORMATION:
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CORGANISM: Homo sapiens
US-09-318-448-11
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                                                    Score 1531.2;
Pred. No. 0;
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Best Local Similarity 99.8%;
Matches 1533; Conservative
; PAGES: 2035-2043
; DATE: 25-MAR-1985
US-09-089-195-1
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/translation="MPVAGSELPRRPLPPAAQERDAEPRPPHGELQYLGQIQHILRC
VRKDDRTGTGTLSVFGMQARYSLRDEFPLLTFRKYFRKGVLBELLKTRGSTNAKEL
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MQLGVPFNIASYALLTYMIAHITGLKFQDFIHTLGDAHIYLNHIEPLKIQLQREPRP
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                                                                       /clone="MGC:22884 INAGE:4048625"
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/clone_lib="NIH_MGC_54"
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1533)
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Submitted (05-FBB-2001) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
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/db_xref="GI:15530267"
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NIH-MGC Project URL: http://mgc.nci.nih.gov
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Pred. No. 1.6e-38;
0; Mismatches 5.
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                                      /organism="Homo sapiens"
/db_xref="taxon:9606"
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Email: cgapbs-r@mail.nih.gov
Location/Qualifiers
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This clone was selected for full length sequencing because it passed the following selection criteria: Similarity but not
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BC013919 1569 bp mRNA linear PRI 10-SEP-2001
Homo sapiens, Similar to thymidylate synthetase, clone MGC:22884
IMAGE:4048625, mRNA, complete cds.
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1 (bases 1 to 1569)
Strausberg, R.
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Anup Madan, Rachel Dickhoff, Jessica Fahey, Stephanie Ford, Julia
Greene, Mark Ketteman and Anuradha Madan
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                                                                                                                                                                                                                                         Length 3298;
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                                                                                                                                                                                                                                         Score 287.2; DB 6;
Pred. No. 2.7e-40;
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709 c 744 g 919 t
Patent: WO 0177389-A 200 18-OCT-2001;
Incyte Genomics, Inc. (US)
Location/Qualifiers
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                                                                                   /organism="Homo sapiens"
/db_xref="taxon:9606"
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
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98.6%;
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Best Local Similarity
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                                                                                                                                                        BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                                                   901
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KEYWORDS
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        JOURNAL
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Gaps

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Length 1569; Indels

CC 961 QY 361 caaagtactaggattacaggcgtgagccaccgcgtccagcgccttggcggttttaatca 	227 Db 361 1021 Qy 421 167 Db 421 1081 Qy 481 107 Db 480 1141 Qy 541	47 Db 540 Qy 601 Db 600 Qy 661 Db 660 FEB-2002 Qy 721 Db 720	QY Db analysis Db	Qy 901 cotcogtccccgccgcgcgcatgctgggcgggctggagctggcggccggc	Qy 1021 tacctggggcagatccaacacatcctccgctggggctcaggaagga
902 ctccgtccccgcccgccacqcctgtgqccggctcggagctggagctccccgccggccccccccgcccg	DB 286 CTCCGTCCCGCCCGCCCGCCATACCTATAACCGAACTACCGAACCTCGAAACTACCGGCCCCCTCGCGCCCGCC		XEYNORDS STATEMENT OF STATEMENT	Epigenomics AG (DE) Cocation/Qualifiers 1180 /organism="synthetic construct" /db_xref="taxon:32630" /note="chemically treated genomic DNA (Homo T 224 a 98 c 347 g 517 t	Query Match 59.7%; Score 708.4; DB 6; Length 1186; Best Local Similarity 75.1%; Pred; No. 8.8e-113; Indels 1; Matches 891; Conservative 0; Mismatches 295; Indels 1; Ge Qy 1 gatcgcgccactgcactccagcctgggtggagagagcggaactctgtctcaaaaaaaa

Unpublished

TITLE JOURNAL

AUTHORS

REFERENCE

human.

ORGANISM

DEFINITION AC020697/c

g

ACCESSION

KEYWORDS VERSION

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19473 TIGTATITITAGTAGAGGGGGGTTTCACCATGTTGTCCAGGCTGGTCTCGAACTCCTG 19414
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     19593 GCTCTGTCGCCCAGGCTGGAGTACAATGGTCGGGATCTTGGCTCACTGCAACCTCTGCCTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  800 others
                                              1440 9151: contig of 7712 bp in length 9152 9251: gap of 100 bp 9252 19650: contig of 10399 bp in length 19651 19750: gap of 100 bp 19751 34038: contig of 14288 bp in length 14038 at 34039 4138: gap of 100 bp 100
                                                                                                                                                                                                                                                                                                                                                                                                                 62654 62753: gap of 100 bp 62754 89313: contig of 26278 bp in length 89032 81913: gap of 100 bp 89132 116606: contig of 27475 bp in length 116607 116706: gap of 100 bp 116707 116742: contig of 49036 bp in length. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11; Indels
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1. .1339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      84.5%; Score 1002.8; DB 2; 96.2%; Pred. No. 1.4e-163; tive 0; Mismatches 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ture 116707 165742
/note="assembly_fragment"
47418 a 35541 c 35457 g 46526 t
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89132. .116606
/note="assembly_fragment
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9252. .19650
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19751. 34038
/note="assembly_fragment"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            47915. .62653
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Homo sapiens"
1340 1439: gap of 10
1440 9151: contig of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /db_xref="taxon:9606"
/chromosome="18"
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47915 62653: cont
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1. .165742
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Matches 1055; Conservative
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ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEATURES
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Birren, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N.,

Barren, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N.,

Barson, S., Baldwin, J., Barna, N., Beckerly, R., Beda, F.,

Boguslavkiy, L., Boukhgalter, B., Brown, A., Burkett, G., Costle, A.,

Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P.,

DeArclano, K., Dewar, K., Domino, M., Doyle, M., Fenestor, J.,

Ferreira, P., Fitzhugh, W., Forrest, C., Gage, D., Galagan, J.,

Gardyna, S., Grant, G., Hagos, B., Haaford, A., Horton, L.,

Howland, J.C., Johnson, R., Jones, C., Kann, L., Kartas, A., Klein, J.,

Landers, T., Lehoczky, J., Levine, R., McGurk, A., McGernan, R.,

Macdonald, P., Marquis, N., McGwan, P., McGurk, A., McKernan, R.,

Macdonald, P., Marquis, N., McGwan, P., McGurk, A., McKernan, R.,

McMpheters, R., Meldrim, J., Meneus, L., Morrow, J., Naylor, J.,

Norman, C. H., O'Connor, T., O'Donnell, P., Ollovar, T. M., Peterson, R.,

Pierre, M., Pisani, C., Pollara, V., Raymond, C., Riley, R., Rothman, D.,

Roy, A., Santos, R., Severy, P., Spencer, B., Stange-Thomann, N.,

Stofanovic, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J.,

Tirrell, A., Vassiliev, H., Viel, R., Vo, A., Wu, X., Wyman, D., Ye, W.J.,

Direct Submission

Apt J., 2000 this sequence version replaced gi:6751720.

All repeats were identified using RepeatMasker:

Smit, A.F.A. & Green, P. (1996-1997)

http://ftp.penome.washington.edu/RW/RepeatMasker:
                                                                                                                                                                                                                   HTG 01-APR-2000
                                                                                                                                                                                 ACO20697

Homo sapiens chromosome 18 clone RP11-145B19 map 18, WORKING DRAFT SEQUENCE, 9 unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Center: Whitehead Institute/ MIT Center for Genome Research
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

    (bases 1 to 165742)

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Quality coverage: 5.9 in Q20 bases; agarose-fp Quality coverage: 5.9 in Q20 bases; sum-of-contigs
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Center clone name: 145 B.19
Center clone name: 145 B.19
Sequencing vector: M13; M77815; 100% of reads
Schemistry: Dye-terminator B1g Dye; 100% of reads
Assembly program: Phrap; version 0.960731
Consensus quality: 160695 bases at least Q40
Consensus quality: 161157 bases at least Q30
Consensus quality: 164107 bases at least Q30
Insert size: 164000; agarose-fp
Insert size: 164000; agarose-fp
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Contact: sequence_submissions@genome.wi.mit.edu
------ Project Information
        1339: contig of 1339 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Birren, B., Linton, L., Nusbaum, C. and Lander, E. Homo sapiens chromosome 18, clone RP11-145B19
                                                                                                                                                                                                                                                                                                                                                                                                                         HTG; HTGS_PHASE1; HTGS_DRAFT
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TITLE

COMMENT

	1021 tacctg 1097 TACCTG	1081	Qy 1141 ggccctg 	RESULT 7 HUMTS1 LOCUS HUMTS1	DEFINITION FOMO SI ACCESSION D00596 VERGION D00596	×	SE	AE NE	COMMENT These Kaneda Kaneda Nation	Mishim Japan Phone: Fax:	FEATURES Source	repeat_unit	repeat_unit prim_transcri	prim_transcrip prim_transcrip	prim_transcrip repeat_unit	repeat_unit exon	CDS	
	1;																-	
BASE COUNT 4521 a 3991 c 4479 g 5605 t ORIGIN	Query Match 98.0%; Score 1163.8; DB 6; Length 18596; Best Local Similarity 99.1%; Pred. No. 3e-191; Matches 1176; Conservative 0; Mismatches 10; Indels 1; Gaps 1	1 gategogocactgoactecagoctgogtgagagagagotagtctctcaaaaaaaaa 60	61 aaaaagaccgccagggctcaaacaaaaaacctcggaaaagccctggcggtctttttttt	121 tttttttttttttttttgggacagtcttgctctgtccggcccaggctggagtacaatggt 180 	181 cggatcttggctcactgcaacctctgcctccaggttcaagcaattcttctgcctcagcc 240	241 tcccaagtagccaccagcccagctaatttttgtanttttagtagagacggggtttcac 300	301 catgitigiccaggetigitetingaacteetgaeeteaggigateeacegeeteggeeee 360	361 caaagtactaggattacaggcgtgagccaccgcgtccagcgccctggcggtttttaatca 420 	421 agtagaaagctgcattataccacttgcttcngttgcnttcagtgagaacgaagaaatgg 480 	481 aaatgcaaatAncttattagttgtaggaaacagatctcaaacagcagttttgtngacaag 540 	541 accgcaggaaaagtgggaactgtgctgctggcttagagaagggcggtcgaccagacgg 600 	601 ttcccaaagggggagtccttccngccaccgcacctgcntccaggttcccgggtntcct 660	661 aagaettteagetgtggeettgggeteegttetgtgeeacaecagtggeteetgagtte 720 	721 ccctggcgcacgctctctagagcggggccgccgqccccgccgacaggaagaggcg 780	781. gagogogggacggoggggaaaaggogogoggaagggtoctgocacogggocacttgg 840 	841 octgoctcogtccogcogogocacttggoctgoctcogtcocgocacttcgcctg 900	901 cctccgtccccgccgccgccatgcctgtggccggctcggagctggcggcgcgcc 960	
BASE	Ou Be	QY Db	QY Db	QY	Q _y	oy .	Qy	Qy Db	Oy Dp	QY	Qy Gp	oy Oy	QY	QY Dp	QY Db	QY	OY do	QΣ

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11 18596 bp DNA linear PRI 14-APR-201 sapiens gene for thymidylate synthase, exons 1, 2, 3, 4, 5, 1 mplete cds.
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Lla; Butheria; Primates; Catarrhini; Hominidae; Homo.
ases 1 to 1859;
la,S., Nalbantoglu,J., Takeishi,K., Shimizu,K., Gotoh,O.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 data kindly submitted in computer readable form by: Sumiko
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Johnson, W.G. and Stenroos, B.Scott.
Methods for diagnosing, preventing, and treating developmental disorders due to a combination of genetic and environmental factor. Patent: US 6210950-A 11 03-APR-2001;
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20-0CT-2000;
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  immunosuppressivė; antiinflammatory; anti-HIV; antibacterial; vulnerary; antiparkinsonian; antisickling; antianaemic; antiarthritic; cancer; antifrheumatic; hepatotropic; cerebroprotective; antiinflammatory; antiallergic; antiidiabetic; antiulcer; anticonvulsant; antifumgal; antiparasitic; cardiant; immune disorder; cardiovascular disorder; neurological disease; infection; nephrotropic; gene therapy; vaccine; ds.
                                                                                                                                                                                                     Human; nootropic; neuroprotective; cytostatic; dermatological; virucide;
  Human nervous system related polynucleotide SEQ ID NO 8929.
                                                                                                    ABA16598/c
ID ABA16598 standard; DNA; 10820
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17-MAR-2000;
18-APR-2000;
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07-JUL-2000;
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11-JUL-2000;
14-JUL-2000;
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                                                                                                                                    ABA16598;
                                                                                        RESULT 15
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AMENGABEL TO AAK64702 encode the human immune/haematopoietic antigen (I) amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic cartivity, and can be used in gene therapy and vaccine production. (I) conteins and polynucleotides may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate (I) expression. For example, they may be used to treat disorders associated with decreased cample, they may be used to treat disorders associated with decreased that affect the activity of (I) by expressing inactive proteins or to cyplement the patients own production of (I). Additionally, (I) to privucleotides may be used to produce the secreted (I), by inserting the nucleic acids into a host cell and culturing the cell to express the clargnose and treat immune/haematopoietic-related diseases, especially cancers and cancer metastases of haematopoietic antigen genomic cancers and cancer metastases of haematopoietic antigen genomic sequences from the present invention. AAK54912 to AAK54950 and AAM82169 very
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nucleic acids encoding human immune/hematopoietic antigen polypeptides, useful for preventing, diagnosing and/or treating cancers and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; SEQ ID NO 34572; 3071pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 20601 BP; 5874 A; 4297 C; 4363 G; 6067 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                  Rosen CA, Barash SC, Ruben SM;
                                                                                                                                                                                                                                                                                                                                                                    (HUMA-) HUMAN GENOME SCI INC
                                2000US-0249245.
   2000US-0249218
                                                   2000US-0249264
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2000US-0249299
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2000US-0254097
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                                                17-NOV-2000;
17-NOV-2000;
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17-NOV-2000;
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                                                                                          4798 TTTTCTTTCTTTTTTTTTTTTTTTTGAGACAGTCTCGCTCTGTCGCCCGGGCTGG 4739
                                                                                                                                                          4738 AdricaAgricaCanagarcrCaGcrCaGcrCaGcrCrCcCGGGCACAAGCAAATTCTG 4679
                                                                                                                                                                                                                        170 agtacaatggtcggatcttggctcactgcaacctctgcctcccaggttcaagcaattct 229
                                                                                                                                                                                                                                                        110 tettittittittittittittittittitgggacagtettgetetgtegecaggetgg 169
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17.2%; Score 203.6; DB 22; Length 20601;
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0; Mismatches 46; Indels
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               Best Local Similarity
Query Match
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4618 TIGIATITITAGIAGAGAC-AGGGITICACCAIGITGGCCAGGCIGGICICGAACICCIG 4560
                            331 acctcaggtgatccacccgcctcggccccccaaagtactaggattacaggcgtgagccac 390
                                                                                                                                                                                            Human; immune; haematopoietic; immune/haematopoietic antigen; cancer; cytostatic; gene therapy; vaccine; metastasis; ds.
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                                                                        4499 TGTGCCCGGCGCTCTGTAGCATTTTCACTTAATAAA 4464
                                                      391 cgcgtccagcgccctggcggtttttaatcaagtaga 426
                                                                                                                      AAK65305 standard; DNA; 22916 BP.
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2000US-0251988. 2000US-0256719.

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2000US-0246528.
2000US-0246532.
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2000US-0249215
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AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (1)
amino acid sequences given in AAM82170 to AAM91921. (1) have cytostatic
activity, and can be used in gene therapy and vaccine production. (1)
proteins and polyuucleotides may be used in the prevention, diagnosis and
treatment of diseases associated with inappropriate (1) expression. For
example, they may be used to treat disorders associated with decreased
expression by rectifying mutations or deletions in a patient's genome
that affect the activity of (1) by expressing inactive proteins or to
supplement the patients own production of (1). Additionally, (1)
cupplement the patients own produce the secreted (1), by inserting
the nucleic acids into a host cell and culturing the cell to express the
protein. (1) proteins and polynucleotides may be used to prevent,
cancers and cancer metastases of haematopoietic-dearied objection
cancers and cancer metastases of haematopoietic artifor genome
cancers and cancer human immune/haematopoietic artifor genome
sequences from the present invention. AAK54942 to AAK54950 and AAM82169
crepresent sequences used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                            Nucleic acids encoding human immune/hematopoietic antigen polypeptides, useful for preventing, diagnosing and/or treating cancers and metastasis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; SEQ ID NO 36572; 3071pp + Sequence Listing; English.
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                                                                               2000US-0251479.
2000US-0251856.
2000US-0251868.
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2000US-0254097
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01-DEC-2000;
05-DEC-2000;
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11-DEC-2000;
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1834 gattgtgccactgcactccagcctgggtgacagagcaagactctatctcaaaaaactaaa 1893

1 gategegecactgeactecagectgggtgagagagagagagatctgtctcaaaaaaaa 60

Score 204.2; DB 22; Length 56743; Pred. No. 1.2e-26; 0; Mismatches 105; Indels 24; Gaps

Query Match 17.2%; Best Local Similarity 71.3%; Matches 320; Conservative C

1894 taaataatgaaaaactcagtgcagatactgggcatctaggtttttct----tttcttttc 1949

aaaaagaccgccagggctcaaacaaaaacctcggaaaagccctggcggtctttttt 120

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1950 tittctttttttttttgagatggagtttcgctctgtcacccaggttggggtacagtggt 2009

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241 toccaagtag-------ccaccacgcccagctaattttgtantttta 2070 toccgagtagctggaattacaggcgcccaccatgcccggctaatttttgtattttta

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                         Human; immune; haematopoietic; immune/haematopoietic antigen; cancer; cytostatic; gene therapy; vaccine; metastasis; ds.
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activity, and can be used in gene therapy and vaccine production. (1)

Cr proteins and polynuclectides may be used in the prevention, diagnosis and
treatment of diseases associated with inappropriate (1) expression. For
example, they may be used to treat disorders associated with decreased

Cr example, they may be used to treat disorders associated with decreased

Cr expression by rectifying mutations or deletions in a patient's genome

that affect the activity of (1) by expressing inactive proteins or to
supplament the patients own production of (1). Additionally, (1)

Cr polynuclectides may be used to produce the secreted (1), by inserting

the nucleic acids into a host cell and culturing the cell to express the

protein. (1) proteins and polynuclectides may be used to prevent.

Cl diagnose and treat immune/haematopoletic-related diseases, especially

cancers and concer metastases of haematopoietic artiges genomic

concers from the present invention. ARK64912 to ARK64703

cr perpendiction and in the present invention. ARK64912 to ARK64920 and AMM82169
                                                                                                                                                                                                                                                                                                    represent sequences used in the exemplification of the present invention.
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KW Human;
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AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I) anticon acid sequences given in AAM82170 to AAM91921. (I) have cytostatic activity, and can be used in gene therapy and vaccine production. (I) proteins and polynucleotides may be used in the prevention, diagnosis casmple, they may be used in the prevention, diagnosis and expression by rectifying mutations or deletions in a partient's genome supplement the Patient's of (I) by expressing inactive proteins or to polynucleotides may be used to produce of (I). Additionally, (I) the nucleic acids into a host cell and culturing the cell to express the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nucleic acids encoding human immune/hematopoietic antigen polypeptides, netastasis .
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                                                                                                08 NOV-2000; 2000US-0246532

08 NOV-2000; 2000US-0246609

08 NOV-2000; 2000US-0246611

08 NOV-2000; 2000US-0246611

17 NOV-2000; 2000US-0249207

17 NOV-2000; 2000US-0249207

17 NOV-2000; 2000US-0249210

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17 NOV-2000; 2000US-0249211

17 NOV-2000; 2000US-0249213

17 NOV-2000; 2000US-0249213
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17-NCV-2000; 2000US-0249265
17-NCV-2000; 2000US-0249295
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17-NOV-2000; 2000US-0249215.
17-NOV-2000; 2000US-0249217.
17-NOV-2000; 2000US-0249218.
17-NOV-2000; 2000US-0249244.
17-NOV-2000; 2000US-0249245.
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                                         2000US-0246525
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2000US-0246609.
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2000US-0251868
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05-DEC-2000;
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05-JAN-2001;
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61 aaaaagaccgccagggctcaaacaaa--aaacctcggaaaagccctggcggtctttttt 118
                                                                                                                                                    119 tttttttttttttttttttgggacagtcttgctctgcccaggctggagtacaatg 178
                                                                                                                                                                                                                                                 Score 204.6; DB 22; Length 11453; Pred. No. 9.8e-27; 0; Mismatches 101; Indels 22; Gaps
                                                                      1 gatogogocactgoactccagoctgggggggggggggggactctgtccaaaaaaaaa 60
                                                                                                                                                                                           179 gtoggatettggeteaetgeaecteeaetgeeteeeaggiteaageaattettetgeeteag 238
                                                                                                                                                                                                                                                                                       280 tagtagagacgggggtttcaccatgttgtccaggctggtctngaactcctgacctcaggt 339
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;
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                                                                                                                                                                                                                                    239 cotoccaagtag-------ccaccacgccaagtagtanttt
Sequence 11453 BP; 3521 A; 2392 C; 2561 G; 2979 T; 0 other;
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ID AAK73271 standard; DNA; 11553 BP.
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72.0%;
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                             Query Match 17.2'
Best Local Similarity 72.0'
Matches 316; Conservative
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24-FEB-2000; 2000US-0184664
02-MAR-2000; 2000US-0186350
16-MAR-2000; 2000US-0186350
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Odnoers and cancer metastases of haematopoietic-derived cells. AAK67769 represent human immune/haematopoietic antigen genomic sequences from the present invention. AAK54942 to AAK54950 and AAM8216 represent sequences used in the exemplification of the present inventi

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5658 ccacgcccagctactttacctttcatatttgtcattattttgtggataataatgaagaat 5717
 gagtgcaatggcacgatctcggctcactgcaacatctgcctcccaggttcaagcaattct 5478
                                                                                                                           5598 gaceteaggtgatetgeetgeeteggeeteegaaagteetgggattacaggeatgageea 5657
                                                                                                                                                                                                     450 tcngttgcnttcagttgagaacgaagaaatggaaatgcaaatAncttattagttgtaggaa 509
                                           cotycotcaycotcocaagtayotaygactacaygcacctyccaccaccaccagctaatt
                                                               tttgtanttttagtagagacgggggtttcaccatgttgtccaggctggtctngaactcct
                                                                                                                                                cogcotcoagcocctggcggtttttaatcaagtagaaaagctgcattatccacttgct
                                                                                                         gacetcaggtgatecaceegeeteggeeeceaaagtaetaggattacaggegtgageea
                                                                                                                                                                                                                                                                                                                                                                        DNA encoding novel human diagnostic protein #20764.
                                                                                                                                                                                                                                                                                                          AAS84960 standard; cDNA; 1539 BP
                                                                                                                                                                                                                                                       5778 gcagctaggtctaagttt 5798
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present invention provides the protein and coding sequences of a number of human reproductive system related antigens. These can be used in the prevention and treatment of reproductive system disorders, including cancer. The present sequence is a genomic sequence encoding a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Isolated nucleic acid molecule encoding a reproductive system antigen is used in preventing, treating or ameliorating a medical condition
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 206.4; DB 22; Length 9731;
Pred. No. 4.8e-27;
0; Mismatches 111; Indels 20;
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11-DEC-2000;
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The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or
Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
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23-AUG-2000; 2000US-0649167.
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Gaps

109 gtctttttttttttttttttttttttttttttttgggacagtcttgctctgtcgcccaggctg 168

17.48; 70.38;

Best_Local Similarity 70.3 Matches 310; Conservative

Query Match

gagtacaatggtoggatcttggctcactgcaacctctgcctcccaggttcaagcaattct 228

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2000US-0225757
2000US-0225758
                                         2000US-0226279
                                             1000US-0226681
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2000US-0246609 2000US-0246610 2000US-0246611 2000US-0246613 2000US-0249208 2000US-0249207 08-NOV-2000; 08-NOV-2000; 08-NOV-2000; 08-NOV-2000; 08-NOV-2000; 08-NOV-2000; 08-NOV-2000; 17-NOV-2000; 01-DEC-2000; 01-DEC-2000; 05-DEC-2000; 05-DEC-2000; 05-DEC-2000; 06-DEC-2000; 08-DEC-2000; 08-DEC-2000; 08-DEC-2000; 08-DEC-2000; 17-NOV-2000; 17-NOV-2000; 17-NOV-2000; 17-NOV-2000; 17-NOV-2000; 05-JAN-2001;

(HUMA-) HUMAN GENOME SCI INC

Ruben SM Rosen CA, Barash SC,

WPI; 2001-483426/52

Nucleic acids encoding human immune/hematopoietic antigen polypeptides, useful for preventing, diagnosing and/or treating cancers and metastasis

Disclosure; SEQ ID NO 20393; 3071pp + Sequence Listing; English.

AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I) amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic activity, and can be used in gene therapy and vaccine production. (I) proteins and polynuclectides may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate (I) expression. For example, they may be used to treat disorders associated with decreased expression by rectifying mutations or deletions in a patient's genome that affect the activity of (I) by expressing inactive proteins or to supplement the patients own production of (I). Additionally, (I) polynucleotides may be used to produce the secreted (I), by inserting the nucleic acids into a host cell and culturing the cell to express the protein. (I) proteins and polynucleotides may be used to prevent, diagnose and treat immune/haematopoietic-derived cells. AAK64703 cancers and cancer metastases of haematopoietic actived cells. AAK64703 cancers and cancer metastases of haematopoietic actived cells. AAK64703 cancers and cancer metastases of haematopoietic actived cells. AAK64703 cancers and cancer invention. AAK54942 to AAK87650 and AAM82169 represent invention. AAK54941 to present invention.

Seguence 56632 BP; 17016 A; 8910 C; 10552 G; 20154 T; 0 other;

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20000S-0226279
20000S-0226681.
20000S-0226868.
20000S-0227182.
20000S-0227009.
                            2000US-0225758
2000US-0225759
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 Cytostatic; immunosuppressive; nootropic; neuroprotective; antiviral; antiallergic; hepatotropic; antidiabetic; antinifammancry; antidicer; vulnerary; anticonvulsant; antidacterial; antifungal; antiparasitic; cardiant; gene therapy; cancer; immune disorder; cardiovascular disorder; neurological disease; infection; human; secreted protein;
                                                                                                                                61 cctccgtcccccgcccgcccgcccgccctgctgtggccggctcggaagttgccgccgccgccggccc 120
                                                                                                                                                            121 ttgccccccgccgcacaggagcgggacgccgagccgcqtccgccgcacgggggagctgcag 180
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04-FEB-2000;
24-FEB-2000;
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07-JUN-2000;
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an analyte in a analyte-binding The present invention relates to a method for assaying an analyte in sample comprising; contacting the sample with a mutant analyte-bind enzyme which has binding affinity for the analyte or an immediate analyte enzymatic conversion product but has attenuated catalytic activity; and detecting resulting binding. The method is useful in monitoring biological systems/processes, or prognosis/diagnosis of disease caused by imbalances of the analytes. The present sequence is a coding sequence used in the present invention. Note: the present sequence is not shown in the specification, but we the specification. using information given in -; 187pp; English. Page from Genbank, Disclosure;

is.

Sequence 18596 BP; 4521 A; 3991 C; 4479 G; 5605 T; 0 other;

ä 120 197 180 257 240 317 300 377 360 420 480 540 919 009 919 099 437 497 556 736 720 961 780 Gaps 9 gategegecactgeactecagectgggtgagagagegagactetgteteaaaaaaaaa 138 aaaaagaccgccagggctcaaacaaaaacctcggaaaagccctggcggtcttttttt ttttttttttttttttttgggacagtcttgctctgtogcccaggctggagtacaatggt toccaagtagccaccacgcccagctaatttttgtanttttagtagagaggggtttcac catgttgtccaggctggtctngaactcctgacctcaggtgatccacccgcctcggccccc catgittgiccaggetggicttgaactectgaceteaggigatecaecegeeteggeeeee cggatettggeteaetgeaacetetgeeteceaggtteaageaattettetgeeteagee caaagtactaggattacaggcgtgagccaccgcgtccagcgccctggcggtttttaatca agtagaaaagctgcattataccacttgcttcngttgcnttcagtgagaacgaagaatgg aaatgcaaatAncttattagttgtaggaaacagatctcaaacagcagttttgtngacaag aaatgcaaatcccttattagttgtaggaaacagatctcaaacagcagttttgttgacaag accgcaggaaaacgtgggaactgtgctgctggcttagaaggcgcggtcgaccagacgg accgcaggaaaacgtgggaactgtgctgctggcttagagaaggcgcggtcgaccagacgg tteceaaagggegeagteetteeengeeaeeggeacetgenteeaggtteeegggtnteet aagactctcagctgtggccctgggctccgttctgtgccacacccgtggctcctgcgtttc 18596; Length Indels 22; Score 1163.8; DB 22 Pred. No. 8.6e-192;); Mismatches 10; 0; 98.0%; ilarity 99.1%; Conservative Similarity Query Match Best Local Simi Matches 1176; \vdash 78 318 378 198 61 121 258 301 181 361 438 421 498 481 557 541 617 601 677 199 737 721 797 QΣ 쉽 a g δž δ 셤 $Q_{\overline{Q}}$ g δŽ υb QΣ QYΩ Qγ g δŽ 셤 QΫ ద δã g ŏ g δŽ Db

The present invention provides a novel method of estimating the susceptibility of an individual to a developmental disorder using genetic and environmental variables. The method can be used in the diagnosis, prevention and treatment of disorders such as schizophrenia, spina bifida cystica, Tourette's syndrom, bipolar illness, autism, conduct disorders, attention deficit disorder, obsessive compulsive disorder, chronic

Disclosure; Page 125-131; 156pp; English.

1080 cotcogteceeegeeegeegeatgeetgtggeeggeteggagetgeegegeeeggeee 1036 genotypes of folate metabolism alleles) fecting an individual and then comparing 900 Human; schizophrenia; developmental disorder; spina bifida cystica; Tourette's syndrome; bipolar illness; autism; conduct disorder; schizophrenia, by forming ds. cotgoctccgtcccgccgccacttggcctgcctccgtcccgccgccacttcgcctg gagegeggaeggeegegggaaaaggegegegeggaaggggteetgeeacegeeacttgg gagogoggacggcggggaaaaggcgcgcgggaaggggtcctgccaccgcgccacttgg cctccgtcccccgccgccgccatgcctgtggccggccggagctgccgccgccgcc cotgootcogtcogcogcogcottggcotgcotcogtcocgcogcogcttcgcotg accggcaccctgtcggtattcggcatgcaggcgcgctacagcctgagaggtgacgccgcg Tourette's syndrome; bipolar illness; autism; conduct disorder; attention deficit disorder; obsessive compulsive disorder; chronic multiple tic syndrome; learning disorder; polymorphism; ggccctgcgggacgggtggcgggaaggaggaggcgcggctgggga 1187 ggcccctgcgggacgggtggcgggaaggagggaggcggctgggga 1263 NO: 11. DENTISTRY Diagnosing a developmental disorder, e.g. datasets (DS) of genetic (e.g. genotypes o and environmental variables affecting an i П Human thymidylate synthase gene SEQ (UYNE-) UNIV NEW JERSEY MEDICINE & ВР AAC91215 standard; DNA; 18596 24-MAY-2000; 2000WO-US14354. 99US-0318448 DS with reference DS (first entry) ES; Stenroos WPI; 2001-025174/03. WO200071754-A1 25-MAY-1999; 20-MAR-2001 Homo sapiens 30-NOV-2000, Johnson WG, AAC91215; these 1097 1157 1141 1217 917 214 1021 781 857 841 901 961 1081 AAC9121 RESULT 셤 δŽ 셤 δŽ g δ g ð 임 ğ 셤 δŽ g

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                pCMVSPORT 6 vector. Library was constructed by Life
Technologies. Contact: Feng Liang Life Technologies, a
division of Invitrogen 9800 Medical Center Drive Rockville
, Maryland 20850, USA Fax: (1) 301 610 8371 Email:
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Bukaryota, Metazoa, Primates, Catarrhini, Hominidae, Homo.

(bases 1 to 935)
Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length.cDMA libraries and normalization
Unpublished (2001)
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279 c 254 g 190 t
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98.2%;
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/issue_type="choriocarcinoma"
/lab_host="DH10B (phage-resistant)"
/host="Organ: placenta; Vector: pOTBT; Site_1: XhoI;
Site_2: EcoRI; cDNA made by Oilgo-dT priming bliectionally cloned into EcoRIXAhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-CDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."
          EST 21-MAR-2001
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                                                                                                                                                                                 Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
BG482405
602526568F1 NIH_MGC_21 Homo sapiens CDNA clone IMAGE:4650280 5',
                                                                                                                                                                                                                                                                                                                                                                                                                                      CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
CNA Sequencing by: Incyte Genomics. Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LINL at:
http://image.llnl.gov
Plate: Lication of column: 17
High quality sequence stop: 524.
                                                                                                                                                                                                                                                       1 (bases 1 to 524)
NIH-WGC http://mgc.nci.nih.gov/.
NIH-WGC http://mgc.nci.nih.gov/.
Dational Institutes of Health, Mammalian Gene Collection (WGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Aproc.
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Pred. No. 2.4e-24;
0; Mismatches 9; Indels 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:4650280"
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/clone="NTZRP3000412"
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/cell_type="teratocarcinoma"
/cell_line="NTZ"
/note="Vector: pME18SFL3; mRNA from NTZ neuronal precursor
cells after 2-weeks retinoic acid (RA) induction"
                                                                                                                                                                                                                                                                                                                                                                                            AU130205 T284-OCT-2000 AU130205 NT2RP3 Homo sapiens cDNA clone NT2RP3000412 5', mRNA
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
Momes 1 to 738)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: genomicsthri.co.jp
HRI human cDNA project; 5'- & 3'-end one pass sequencing: Helix
Research Institute; CDNA library construction: Department of
Virology, Institute of Medical Science, University of Tokyo, and
              tgeegegegegegetgeeeccegegegeacaggaagggggaegeegageegegteegeege 1006
                                                                                                                                                                          1067 acgaccgcacgggcaccggcaccctgtcggtattcggcatgcaggcgcgctacagcctga 1126
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Yamamoto,J., Wakamatsu,A., Nakamura,Y., Nagai,T., Sugano,S. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             181 ACGGGGAGCTGCAGTACCTGGGGCAGATCCAACACTCCTCCGCTGCGGCGTCAGGAAGG 240
                                                     121 recedecedecetrrecececececedacases accedecedececerecece 180
                                                                                                                                                                                                                   241 ACGACCGCACGGCCACCGCCACCCTGTCGGTATTCGGCATGCAGGCGCGCTTCAGCCTGA 300
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Pred. No. 2.5e-26;
0; Mismatches 2; Indels
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1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
Tel: 81-438-52-3951
Fax: 81-438-52-3952
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/db_xref="taxon:9606"
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Genomics Laboratory
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99.3%;
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Matches 297; Conservative
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/db_xref="taxon:9606"
/db_xref="taxon:9606"
/clone="CSDD160FDED#06"
/tlssue_type="Placenta"
/tlssue_type="placenta"
/tlssue_type="placenta"
/note="Yector: pcWxSPRT 6; Site_1: NotI; lst strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the pcWxSPRT 6 vector. Library was normalized. Library was constructed by Life Technologies. Contact: Feng Liang Life Technologies, a division of Invitrogen 9800 Medical Center Drive Rockville, Maryland 20850, Usa Fax: (1) 301 610 8371
Email: fllang@lifetech.com URL:
http://fullength.invitrogen.com"
0.2 a 288 c 259 g 188 t lothers
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                                                                                                        1000 ccgccgcacggggagctgcagtacctggggcagatccaacacatcctccgctgcggcgtc 1059
                                                                                                                                                                              880 cccgccgccacttcgcctgcctccgtcccccgccgccgccgccatgcctgtggccggc 939
                                  61 eccecececeacararesecraceraceaceaceaceaceaceaceacearecareacease 120
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BP 191 91006 EVRY cedex - France
Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
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Pred. No. 2.5e-27;
0; Mismatches 2;
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AL551990
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